

GenCore version 4.5
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OK nucleic - nucleic search, using sw model

Run on: April 4, 2002, 20:28:25 ; Search time 2158.35 Seconds
(without alignments)
9404.766 Million cell updates/sec

Title: US-09-775-879-20
Perfect score: 1889
Sequence: 1 gaagatcgatcaatcaatca.....aaatgttgatgattcttgc 1889

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues
Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estfun:*
2: em_esthum:*
3: em_estio:*
4: em_estio:*
5: em_estio:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_hrc:*
10: gb_est1:*
11: gb_est2:*
12: gb_hrc:*
13: gb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rtd:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	478	25.3	498	13	AA011450 F27K177FC
2	183.6	9.7	583	11	BE425767 sra2f04.y
3	182	9.6	716	10	AM775288 EST334353
4	182	9.6	804	11	BI308419 EST529829
5	181.8	9.6	535	10	AM596303 sjo1f11.y
6	181.4	9.6	592	10	AM219366 EST301848
7	175.6	9.3	447	10	BE459711 EST415003
8	173.8	9.2	667	11	BE357415 DGL15.H1
9	173.4	9.2	621	11	BE123510 EST169146
10	170.2	9.0	722	11	BE398293 EST496971
11	169.6	9.0	464	10	AM040702 EST283566
12	168.8	8.9	708	10	BE602261 HVSMEH009

13	168	8.9	597	11	BE098248	B3098248	EST462767
14	167.2	8.9	708	11	BE601702	BE601702	HVSMEH009
15	166.6	8.8	782	11	BE624091	BE624091	HVSMEH000
16	166	8.8	672	11	BE600842	BE600842	EST505737
17	165	8.7	668	11	BE404301	BE404301	WHE1204.F
18	165	8.7	781	11	BE617574	BE617574	HVSMEC001
19	162.2	8.6	497	10	AM065645	AM065645	614056G01
20	162.2	8.6	606	10	AT195645	AT195645	614004G03
21	162.2	8.6	840	11	BE320935	BE320935	Zm04_02e0
22	161.8	8.6	605	11	BE417093	BE417093	949053A09
23	160.6	8.5	700	10	AM680178	AM680178	WS1_4.B01
24	159	8.4	668	11	BE586763	BE586763	FM1_30_A1
25	158	8.4	570	11	BE933493	BE933493	WS1_4.B01
26	157.4	8.3	478	10	AT941789	AT941789	618035C05
27	156.8	8.3	427	11	BE316184	BE316184	saf62402.
28	155.8	8.2	544	10	AT629882	AT629882	486041E07
29	155.8	8.2	671	11	AT857158	AT857158	603007C02
30	155	8.2	587	11	BE586850	BE586850	FM1_30_A1
31	154.8	8.2	620	10	AT621765	AT621765	486019E06
32	151.2	8.0	618	10	AM498324	AM498324	660046C01
33	149.8	7.9	538	11	BE487658	BE487658	EM1_65_G0
34	147.2	7.8	362	11	D33996	D33996	RI0R0753A.R
35	145.8	7.7	661	10	BE413481	BE413481	MC6010.D0
36	145.2	7.7	562	10	BE125051	BE125051	DG1_15.H1
37	145	7.7	567	10	AM429266	AM429266	EST306722
38	135	7.1	825	10	BE643026	BE643026	Cr12_7.L0
39	126.4	6.7	540	10	AT947832	AT947832	603029C07
40	124.8	6.6	541	11	BE322635	BE322635	EM1_41.D0
41	124.6	6.6	572	10	BE471514	BE471514	EST416367
42	122.8	6.5	486	11	BE358931	BE358931	949053A09
43	121.6	6.4	551	10	BE471892	BE471892	EST416745
44	120.4	6.4	483	10	AM700015	AM700015	gb37c07.Y
45	118.2	6.3	415	11	BE071337	BE071337	C055P67U

ALIGNMENTS

RESULT 1
AA011450/c 498 bp DNA 29-MAY-1998
LOCUS F27K177FC IGF Arabidopsis thaliana genomic clone F27K17, DNA
DEFINITION sequence.
ACCESSION AA011450 GI:3166695
VERSION
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 498)
Rounsley,S.D., Suh,E.J., Wible,C., Golden,K., Jatsman,S., Choi,P., Yu,K., Akhretovye,B., Shen,K., Goonasekaram,S., Millscher,J., Adams,M.D. and Venter,J.C.
A BAC End Sequence Database for Identifying Minimal Overlaps in Arabidopsis genomic Sequencing. Update 4
Unpublished (1998)
Contact: Steve Rounsley
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: rounsley@tigr.org
Seq primer: M13-21
Class: BAC ends
High quality sequence stop: 498.
Location/Qualifiers
1..498
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"

FEATURES

source

/clone="f27k17"
/clone_lib="TGF"
/sex="hermaphrodite"
/note="Vector: Belopacili; Site_1: EcoRI; Site_2: EcoRI;
Produced by Thomas Altmann"
BASE COUNT 200 a 95 c 83 g 120 t
ORIGIN

Query Match 25.3%; Score 478; DB 13; Length 498;
Best Local Similarity 98.8%; Pred. No. 2,5e-81;
Matches 492; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
QY 363 ccaaaagctcgcagcttcacttccttgaatcactatgccttaacgccttccttaagtcg 422
DB 498 CCAAGGCTCGACTTCACCTTGTATTCACATTCCTTAATGCTTATGATATCG 439
QY 423 atttttaattt-aagaagaagggttcctgcgtgactgacgaatatttgattgattg 481
DB 438 ATTTTCAATTTAAGCAAGAGGGTTCCTGCTACTGTAAGTAATTTGATTTGATG 379
QY 482 tggatagtcactgttcgacttattgattgactgacatccatccatgaaggattga 541
DB 378 TGATATTCTCATGTTTCATTTATTTGATTTATTTGATTTCCATTAAGGATTTGA 319
QY 542 acagtagtggtctataaagtttttgcaaaccaatgagaagtcgtacatcttgaagt 601
DB 318 ACAGTTAGTGGCTATTAATGATTTTGTGCACCAATGAGAGTGTACATCTTTGAAGT 259
QY 602 tgaatttcaactgcatcttaagtcacttaaatgttttgtaagtgatgtcactc 661
DB 258 TGAATTTTCACTTGCATTTAAGTCCACTTAATTTGTTGTAAGTGTCTACTT 199
QY 662 tcaagacatctcttctcgtctcctgaagctcgtccttaagtggaatccttctt 721
DB 198 TCAGACACATTTCTTTCTGCTTCTGAGACCTGCTTGTGTAATTTGATTTGCT 139
QY 722 ctgttttgctcagaatgcacttcctacaataaaggctatgcgtttgcaaatgtttg 781
DB 138 CTGTTTGTCTTCACATTCATTTCTCAATTAAGCTATGCGTTGCAAAATGTTGTCG 79
QY 782 aatgaagcctatgcctgctgaactcttctcgaactgctcgaaggtatgattgaag 841
DB 78 AATGAAGCTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 19
QY 842 tggctgaccacaatgttct 859
DB 18 TGGTTGACCAATGTTT 1
RESULT 2
BF425767 583 bp mRNA EST 28-NOV-2000
LOCUS BF425767.1 GI:11413756
DEFINITION Gm-c1051-728 5' similar to TR:Q9ZT29 Q9ZT29 SIEROL-C5(6
)-DESATURASE.; mRNA sequence.
ACCESSION BF425767
VERSION BF425767.1
KEYWORDS soybean.
SOURCE Glycine max.
ORGANISM Glycine max.
REFERENCE 1 (bases 1 to 583)
AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpeliding,J., Correll,V., Khanna,
A., Bolla,B., Matra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wyle,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,
Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,
R., Ritzer,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,
R., Waterston,R. and Wilsson,R.
TITLE Public Soybean EST Project

JOURNAL Unpublished (1999)
COMMENT Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
High quality sequence stop: 393.
Location/Qualifiers
1..583
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1051-728"
/clone_lib="Gm-c1051"
/tissue_type="floral meristematic mRNA"
/lab_host="DH10b"
/note="Vector: Bluescript II SK+; Site_1: EcoRI; Site_2:
XhoI. The cDNA library was constructed from floral
meristematic mRNA provided by Dr. Halina Knap of Clemson
University. Complementary DNA was synthesized from mRNA
using a primer consisting of a poly(dT) sequence with a
XhoI restriction site. EcoRI adapters were ligated to the
blunt-ended cDNA fragments followed by XhoI digestion. The
cDNA fragments were directionally cloned into the
EcoRI-XhoI restriction site of the Bluescript vector. The
ligated cDNA fragments were transformed into DH10b host
cells (GibcoBRL). This library was constructed in the
laboratory of Dr. Randy Shoemaker."

BASE COUNT 131 a 149 c 120 g 183 t
ORIGIN
Query Match 9.7%; Score 183.6; DB 11; Length 583;
Best Local Similarity 71.1%; Pred. No. 2.7e-25;
Matches 243; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
QY 720 gtctgttctcagatgcataatccctacaataaaggctatgcgtttgcaaatgtttg 779
DB 203 GTTATGTTCCCAAGATGCTATTCCTCTCGAAGAGCCATGCTTCAAAATATCTGTT 262
QY 780 gcaatgaagcctatgcctgctgaactcttctcgaactgctcgaaggtatgattgaag 839
DB 263 GCTATGAAGCCATGCTTGTGATCACTTGTCTCAACTGTTTGGAGTACTGTGTAAGA 322
QY 840 ctgttctgaccacaatgttctcagatgcataaagcgaatcggctggaattcgtattt 899
DB 323 ACTGCGCTGACAAAGGCTATCTAGATTAATGATGTTGGTGGCTTGCATTCCTGTTG 382
QY 900 taactgcacatcactctgttcttgcgtgagtttgatattatgtagaagaagaagctc 959
DB 383 TATTAGCAATTTATCTAAGATTTGATGAGTTGTATTATTTGATGACACAGAACTG 442
QY 960 catgacatgaagcctcctataaaglatcctacatccacccatcatcatcaacaag 1019
DB 443 CACGACATAAACCGCTTTACAAATATCTTATCTACCCATCTACATTAATAACAG 502
QY 1020 aatacactctcactatgcgcgtaagtgatttcaagttgt 1061
DB 503 AACACTGCTCCCTTGTGCTGTTGGCATTTTCATCTCTT 544
RESULT 3
AM775288 716 bp mRNA EST 07-SEP-2000
LOCUS AM775288
DEFINITION EST334353 D5L1 Medicago truncatula cDNA clone pDIL-1EL1, mRNA
sequence.
ACCESSION AM775288

KEYWORD	AW775288.1	GI:7765101
SEQUENCES	EST.	
SOURCE	barrel medic.	
ORGANISM	Medicago truncatula	
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.	
REFERENCE	1 (bases 1 to 716)	
AUTHORS	Fedorova,M., Pierson,B.L., Samac,D.A., Vance,C.P., Gent,G.S., Peng,H., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.M.	
TITLE	ESTs from leaves of Medicago truncatula after inoculation with Colletotrichum trifolii	
JOURNAL	Unpublished (2000)	
COMMENT	Contact: Deborah A. Samac Department of Plant Pathology University of Minnesota 495 Borling Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA Tel: 612 625 1243 Fax: 651 649 5058 Email: debbye@puccini.crl.umn.edu Minnesota sequence name:M358621e TIGR sequence name:MTFAA257K More information is available at: http://chrystle.tamu.edu/medicago Seq primer: SKmod (CTA gaa CTA gta gat CC).	
FEATURES	Location/Qualifiers	
source	1..716	
	/organism="Medicago truncatula"	
	/cultivar="genotype A17"	
	/db_xref="taxon:3880"	
	/clone="pDSIL1e1"	
	/clone_id="DSIL"	
	/tissue_type="leaves infected with Colletotrichum trifolii"	
	/dev_stage="cotyledons and primary leaves harvested 5 and 8 days after inoculation with Colletotrichum trifolii"	
	/lab_host="E. coli strain XLOLR"	
	/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA from cotyledons and primary leaves harvested 5 and 8 days after inoculation with Colletotrichum trifolii. The cDNA was directionally ligated into the uni-ZAP XR vector from StrataGene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant Lambda-ZAP phage using Ex-Assist helper phage and propagated in XLOLR cells. Note: EST may be of fungal origin."	
BASE COUNT	187 a 162 c 112 g 255 t	
ORIGIN		
Query Match	9.6%; Score 182; DB 10; Length 716;	
Best Local Similarity	70.8%; Pred. No. 5.3e-25;	
Matches 242; Conservative	0; Mismatches 100; Indels 0; Gaps 0;	
0Y	720 gtcgttttgcctcagatgcgaatccctccacaataaagctagcgtttgcaaatgtttgtg 779	
Db	296 gttttatgtccctaaagatccatccacatccatgaagccattcttgcaaatatcgggtt 355	
0Y	780 gcaatgaagcgtacatcagtgtaacctctctcgaactgctcgaagatgattgaa 839	
Db	356 ACAATGAAGAAGAAATCCCTTGCTGTATATGTTGCTTCCAACTATTTCTGAGTGCTGTAG 415	
0Y	840 cgtgttgtagccaaatgtttgtcagcatagacgaatctgcgtgattctgtattt 899	
Db	416 CTTGGCTGGACAAATCCCTTGCTGTAGAAATTAATCTTGCTTGGAATGCCATCAATGGT 475	
0Y	900 tacatgcgcattcatctgttttgcgttgatgttgattattatgtagacagaagctt 959	
Db	476 TATTTAGCAATTTATATGTTATTTCTTAAGATTTGGTATTATTATTTGGATGATGCAATGAAGTTG 535	

0y	960	catgacaltagaccctctcatataagatcatctccatgcaccccatcatcatctacacagaagcag	1019
Db	536	CATTGACATTAATAAACCCCTTTTACAATAATCTCTCAAGAACACATCACTACATTAATAACAA	595
0y	1020	aatacacctctccattgcgcgtaagtgcttttcagttgtc	1061
Db	596	AATACTCTCTCTCCCATTTGCTGTGGCTTTTCATCTCTT	637
RESULT	4		
LOCUS	BI308419		
DEFINITION	BI308419	804 bp	mRNA
ACCESSION	ES1529829	GP0D	Medicago truncatula cDNA clone pg:OD-SD24 5' end.
VERSION	BI308419		
KEYWORDS	EST.		
SOURCE	BI308419.1	GI:14982746	
ORGANISM	barrel medic.		
	Medicago truncatula		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;		
	Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;		
	Medicago.		
REFERENCE	1	(bases 1 to 804)	
AUTHORS	Grusak, M.A., Samac, D.A., Town, C.D., Van Aken, S., Utterback, T., Cho, J., and Fraser, C.M.		
TITLE	ESTs from developing reproductive tissues of Medicago truncatula		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Michael A. Grusak USDA/ARS Children's Nutrition Research Center Baylor College of Medicine 1100 Bates Street, Houston, TX 77030-2600, USA Tel: 713-798-7044 Fax: 713-798-7078 Email: mgrusak@bcm.tmc.edu B395274e TIGR sequence name: WMOAP24TK More information is available at: www.medicago.org Seq primer: SKmod (CTA GAA CTA gct gAT CC). Location/Qualifiers 1..804 /organism="Medicago truncatula" /cultivar="A17" /db_xref="taxon:3880" /clone="pgPOD-SD24" /clone_11b="GP0D" /tissue_type="Immature pod walls" /dev_stage="Immature pods, ranging in age from 15 to 30 days after pollination" /note="vector: phuescript SK-, Site_1: EcoRI; Site_2: XhoI; Immature pods, ranging in age from 15 to 30 days after pollination, were collected from greenhouse-grown plants. At harvest, seeds were removed from pods and isolated pod walls were collected and immediately frozen in liquid nitrogen. Pod walls were pooled for mRNA extraction. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap III vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-sistit helper phage and propagated in XL0LR cells."		
FEATURES	source		
BASE COUNT	228 a	167 c	137 g 272 t
ORIGIN			
Query Match	9.6%	Score 182;	DB 11; Length 804;
Best Local Similarity	70.8%;	Pred. NO. 5.2e-25;	
Matches 242;	Conservative 0;	Mismatches 100;	Intels 0; Gaps 0;
0y	720	gtctgttttgcctcagatgcgaatctccatacaaaagcgtacgtctttgcaaatgtttg	779
Db	241	GTTTATGTCTCCAAAGAGCCATTCATTCACATGTGACACATCTGTGCAAAATATCGTT	300

[illegible]

RESULT	5
AW596303	
LOCUS	AW596303
DEFINITION	AM596303 535 bp mRNA EST 18-JUL-2000 gaj01f11.y1 Gm-cd1032 Glycine max CDNA clone GENOME SYSTEMS CLONE ID: sj010332-646 5' similar to TR-Q97T29 Q97T29 STEEROL-C5(6)-DESATURASE.; mRNA sequence.

ACCESSION	AW596303	GI:7283699
VERSION	AW596303.1	
KEYWORDS	EST.	
SOURCE	soybean,	
ORGANISM	Glycine max	

Euraryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 535)		
Shoemaker, R.	Kelm, P., Voklin, L., Expelding, J., Corcell, V., Khanna	
Wyllie, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,		
Wyllie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers		
Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk		
R., Ritters, E., Kohn, S., Shlin, T., Jackson, Y., Cardenas, M., McCann		
R., Waterston, R. and Wilson, R.		
		Public Soybean EST Project

JOURNAL
COMMENT

Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
Insert length: 1224 Std Error: 0.00
High quality sequence stop:360.

FEATURES
source

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/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1032-646"
/clone_id="Gm-c1032"
/lssue_type="Cotyledons of 8-day-old 'Williams' seedlings"
/lab_host="Dh103"
/notice="Vector: pBluescript II XR; Site.1: EcoRI; Site.2: XhoI. This cDNA library was constructed from mRNA isolated from cotyledons of 8-day-old 'Williams' seedlings which were propagated on paper towels with distilled water for 5 days (etiolated), then greenhouse grown for 5 days in

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potting soil. The cotyledons were flash-frozen in liquid nitrogen. Stratagene's cDNA Synthesis Kit (catalog number 200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5'-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nucleotide (V=A, C, or G) was added to the 3' end of the primer (GAGACGAGACGACGACGACGACACTCTTCGAC(TT)18V) to anchor the primer at the 5' end of the poly(A) tract. After second strand synthesis, the cDNA ends were filled in with cloned Pfu DNA, ligated to EcoRI adapters and subsequently phosphorylated. The cDNA was then precipitated and redissolved in sterile, RNase-, DNase-free water. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI from Promega (400U/ul); all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500 bp cutoff, using GIBCOBRL Life Technologies' cDNA Size Fractionation column. The column eluent was then precipitated, redissolved, and ligated into Stratagene's pBluescript II XR Predigested vector (pBluescript II SK(+)) vector that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene). 1008 of the white and 87.58 of the blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=28 and 8 respectively). This library was constructed by Dr. Paul Kelm and Dr. Virginia Coryell."

Query Match	9.6%	Score	181.8	DB	10	Length	535
Best Local Similarity	71.4%	Pred. No.	5.9e-25				
Matches	237	Conservative	0	Mismatches	95	Indels	0
						Gaps	0

720 gtcctgttttccttcagatgcgaattcctacaacaataagcgcatgcgtttgcaaatgtttcgcg 779

QY 780 gcaatgaagcctatgccaatggtacactctcttcccaactgctccgagagtatgattgaa 839

Db 263 GCTATGAAGCCATGCCCTTGCTACACTTTCCTTCCAACTGTTCCGAGTACCTGGTAGAA 322

Db 323 ACTGCTGGACAAAGTGCATTCCTTAATTAATGTTGGTTCCTTGCAATACCTTGTG 382

QY 900 tacatcgcatctatcttctgttgcgttatctgttatcttgaaatgcacagagagctc 959

[illegible]

Db 443 CAGGACATAAACCGCTGACAAATATCTTCATGCTACCCATCAGACTCTACNATAACAG 502

09 1020 aatacactctctccacattgcgcgtaagtgctt 1051
||| ||| ||| ||| ||| ||| ||| ||| |||
503 tttgttcctctctctctctctctctctctctctctt 534

AM219366					
LOCUS	592 bp	mRNA	EST	18-MAY-2001	
AM219366					

Lycopersicon esculentum cDNA clone cLEX4M9, mRNA sequence.
AW219366

KEYWORDS EST, tomato, source

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

TITLE
JOURNAL
COMMENT

,L.H.
An EST database from Sorghum: dark-grown seedlings
Unpublished (2000)
Contact: Cordonnier-Pratt MM
Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
Email: mmpatr@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: JEN REV
High quality sequence stop: 593
POLYA-NO.

FEATURES
source

location/Qualifiers
1..667
/organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone_lib="Dark Grown 1 (DG1)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was
made from poly-A RNA in the cloning vector Lambda Zap II.
Clones to be sequenced were prepared by mass excision."
BASE COUNT 147 a 179 c 165 g 176 t
ORIGIN

Query Match 9.28; Score 173.8; DB 10; Length 667;
Best Local Similarity 71.3%; Pred. No. 1.9e-23;
Matches 229; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

Y 734 aggtgcaatctccacaataaaggatcgcttgcaaatcttggtgcaatgaagctat 793
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Db 293 AGATGCCATTCCCAATAAGCTATGAAGAACCAATAGTTTACATCGAAGGCTAT 352
Y 794 gcaatgtaactctctctcaactgctcgcgagagatgatgaacgttgtagacaa 853
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Db 353 GCCCTTTTAACTGCTCTCCCACTTATCATATGATATGATGAGAGCGATGACCA 412
Y 854 atgtttgcagcaataaagcaatcgctgagatctgattcttaccatcgcaacta 913
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Db 413 GTGTACTTAAATACAGTAGAGTGGTGTTCATATACCTCTTATATGCTATCTA 472
Y 914 tctgttctcgctgagcttggtatcttgaatgcacagagcttaccatgaagcc 973
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Db 473 TCCCATTTTGTGAGAGTTTGGAATTTACTGATGCACAGACAGTTGATGACATAAAGCC 532
Y 974 tctctaaaglatctccatccaccatcatatctacaacaagacatacatctctcc 1033
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Db 533 ATTATACAAATATCTGCATCAACCCATCATATTTCACACAGAAATATCTTGTCTCC 592
Y 1034 attgcggtgaagtgattca 1054
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Db 593 ATTTGCTGACTTGCAATTTC 613

RESULT 9
BG123510 621 bp mRNA EST 31-JAN-2001
LOCUS BG123510
DEFINITION EST469146 tomato shoot/meristem Lycopersicon esculentum cDNA clone
cTOF2K3 5' sequence similar to nearly identical to Nicotiana
tabacum sterol-C5(6)-desaturase, mRNA sequence.

ACCESSION BG123510
VERSION BG123510.1 GI:12623688
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.

REFERENCE 1 (bases 1 to 621)
AUTHORS van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Uterback,T.,
Hansen,C., Ronning,C. and Tanksley,S.
TITLE Generation of ESTs from tomato shoot/meristem tissue
JOURNAL Unpublished (2001)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>.

FEATURES
source

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/cultivar="TA496"
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/clone_lib="cTOF2K3"
/clone_lib="tomato shoot/meristem"
/tissue_type="shoot/meristem"
/dev_stage="developing shoots from 4-6wks old plants"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; Small expanding leaves from the growing tip were
taken from greenhouse plants (4-6wks old TA496). Tissue
was immediately frozen in liquid nitrogen."
BASE COUNT 163 a 137 c 126 g 195 t
ORIGIN

Query Match 9.28; Score 173.4; DB 11; Length 621;
Best Local Similarity 69.9%; Pred. No. 2.3e-23;
Matches 234; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

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Y 840 cgtgttggaacaaatgttgctgacatagaacatggtgagatcttgattgtc 899
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Db 320 AACGATGAGACCAATGTTTGGAGATGATGATGATGATGATGATGATGATGATC 379
Y 900 tacatgcacatctatctgttcttgctgagcttggtatcttgaatgacaaagaagct 959
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Db 380 AATCGGCTATTATCTTGTATATGATGATGATGATGATGATGATGATGATGATG 439
Y 960 catgacatgaagcctctctataaglatctccatgcacacatcatatctacaagaag 1019
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Db 440 CATGACATTAACCTCTGTATTAATATCTGCATCTACATCATATTTCACACAAAGCA 499
Y 1020 aatacatctctccatcttgccggtgaagtgattca 1054
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Db 500 AACACACTTTCCTCCATTGCTGAGTGGCATTTCA 534

RESULT 10
BG598293 722 bp mRNA EST 12-APR-2001
LOCUS BG598293
DEFINITION EST496971 cSTS Solanum tuberosum cDNA clone cSTS20L7 5' sequence,
mRNA sequence.

ACCESSION BG598293
VERSION BG598293.1 GI:13616433
KEYWORDS EST.
SOURCE potato.
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 722)
van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Chieningo,A.,
Bouffard,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B.

Mon Apr 8 17:54:16 2002

us-09-775-879-20.rst

Page 10

Search completed: April 5, 2002, 04:25:21
Job time: 28616 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 5, 2002, 03:25:38 ; Search time 89.32 Seconds
(without alignments)
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Title: US-09-775-879-20

Perfect score: 1889

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IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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1	60	3.2	7218	1 US-08-232-463-14	Sequence 14, Appl
2	48	2.5	240	1 US-08-628-417-6	Sequence 6, Appl
3	46.4	2.5	1117	4 US-09-247-373B-33	Sequence 33, Appl
4	46.2	2.4	1582	3 US-08-545-196B-10	Sequence 10, Appl
5	46.2	2.4	1582	3 US-08-545-196B-12	Sequence 12, Appl
6	45.6	2.4	2223	1 US-08-257-073-4	Sequence 4, Appl
7	44.6	2.4	5394	3 US-08-688-376-1	Sequence 1, Appl
8	44.2	2.3	144	1 US-08-702-344-26	Sequence 26, Appl
9	42.8	2.3	12980	3 US-08-811-566-5	Sequence 5, Appl
10	42.2	2.2	2447	2 US-09-014-969-14	Sequence 14, Appl
11	42	2.2	124	6 5185243-1	Patent No. 5185243
12	41.8	2.2	260	2 US-08-520-678A-29	Sequence 29, Appl
13	41.8	2.2	260	4 US-08-897-126-29	Sequence 29, Appl
14	41.6	2.2	356	2 US-08-520-678A-22	Sequence 22, Appl
15	41.6	2.2	356	4 US-08-897-126-22	Sequence 22, Appl
16	41.6	2.2	9646	1 US-08-811-566-1	Sequence 1, Appl
17	41.4	2.2	140	1 US-08-628-417-5	Sequence 5, Appl
18	41.2	2.2	3527	2 US-08-909-965C-7	Sequence 7, Appl
19	41	2.2	1733	3 US-09-073-569-1	Sequence 1, Appl
20	40.8	2.2	1411	4 US-08-964-127-5	Sequence 5, Appl
21	40.8	2.2	1813	4 US-09-071-224-3	Sequence 3, Appl
22	40.6	2.1	270	2 US-08-520-678A-30	Sequence 30, Appl
23	40.6	2.1	270	4 US-08-897-126-30	Sequence 30, Appl
24	40.4	2.1	1066	1 US-08-157-101A-4	Sequence 4, Appl
25	40.4	2.1	6671	1 US-08-280-443-1	Sequence 1, Appl
26	40.4	2.1	6671	1 US-08-457-459-1	Sequence 1, Appl
27	40.4	2.1	6671	1 US-08-555-678-1	Sequence 1, Appl

C 28	40.4	2.1	6671	5 PCT-US95-02275-1	Sequence 1, Appl
C 29	40.2	2.1	361	4 US-09-018-584A-9	Sequence 9, Appl
C 30	40.2	2.1	1051	4 US-09-245-041-10	Sequence 10, Appl
C 31	40	2.1	1098	3 US-09-248-335-35	Sequence 35, Appl
C 32	40	2.1	1493	1 US-08-340-820-24	Sequence 24, Appl
C 33	40	2.1	1493	1 US-08-593-535-24	Sequence 24, Appl
C 34	39.6	2.1	19124	2 US-08-487-826B-13	Sequence 13, Appl
C 35	39.6	2.1	1882	4 US-09-370-253-1	Sequence 1, Appl
C 36	39.2	2.1	253	2 US-08-520-678A-25	Sequence 25, Appl
C 37	39.2	2.1	253	4 US-08-897-126-25	Sequence 25, Appl
C 38	39.2	2.1	790	4 US-09-363-970-4	Sequence 4, Appl
C 39	39.2	2.1	1683	4 US-09-347-803-11	Sequence 11, Appl
C 40	39.2	2.1	1700	2 US-08-897-340-14	Sequence 4, Appl
C 41	39.2	2.1	1700	2 US-08-252-329-4	Sequence 4, Appl
C 42	39.2	2.1	1921	2 US-08-557-128-11	Sequence 11, Appl
C 43	39	2.1	9589	1 US-07-925-695-1	Sequence 1, Appl
C 44	39	2.1	9589	1 US-07-925-695-2	Sequence 2, Appl
C 45	38.6	2.0	1474	4 US-08-821-994-64	Sequence 64, Appl

ALIGNMENTS

RESULT 1
US-08-232-463-14
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHIEFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
CLASSIFICATION: 435
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZ9pt-F15
US-08-232-463-14


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; Sequence 10, Application US/08545196B
; Patent No. 6080577
; GENERAL INFORMATION:
; APPLICANT: MELKI, JUDITH
; APPLICANT: MONNICH, ARNOLD
; TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
; TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,196B
; FILING DATE: 19-OCT-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FARACI, C. J.
; REGISTRATION NUMBER: 32,350
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1582 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-545-196B-10

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Best Local Similarity 56.1%; Pred. No. 0.0061;
Matches 87; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

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; Sequence 12, Application US/08545196B
; Patent No. 6080577
; GENERAL INFORMATION:
; APPLICANT: MELKI, JUDITH
; APPLICANT: MONNICH, ARNOLD
; TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
; TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
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; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,196B
; FILING DATE: 19-OCT-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FARACI, C. J.
; REGISTRATION NUMBER: 32,350
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1582 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-545-196B-12

Query Match          2.4%; Score 46.2; DB 3; Length 1582;
Best Local Similarity 56.1%; Pred. No. 0.0061;
Matches 87; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

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QY 1780 gtctcttctctctctctctatcagtcgtctcctcaaccttccaattatgtta 1839
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RESULT 6
US-08-257-073-4/c
; Sequence 4, Application US/08257073
; Patent No. 576597
; GENERAL INFORMATION:
; APPLICANT: Paolletti, Enzo
; APPLICANT: de Taisne, Charles
; APPLICANT: Tine, John A.
; TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue, 25th Floor
; CITY: New York
; STATE: New York
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/257,073
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/075,783
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

CM nucleic - nucleic search, using sw model

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Title: US-09-775-879-20

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Total number of hits satisfying chosen parameters: 1861242

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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	158.2	8.4	446	21	AAH5689
4	134.6	7.1	936	22	AAAF8252
5	134.6	7.1	936	22	AAAF8254
6	134.6	7.1	936	22	AAAF8257
7	134.6	7.1	936	22	AAAF8259
8	134.6	7.1	936	22	AAAF8262
9	134.6	7.1	936	22	AAAF8255
10	133.8	7.1	936	22	AAAF8252
11	133.8	7.1	936	22	AAAF8254

12	133.8	7.1	936	22	AAAF8257	Oligonucleotide D1
13	133.8	7.1	936	22	AAAF8259	Oligonucleotide D2
14	133.8	7.1	936	22	AAAF8252	Oligonucleotide D1
15	133.8	7.1	936	22	AAAF8255	Oligonucleotide D1
16	54.2	2.9	1954	21	AAAZ3441	cDNA encoding huma
17	52.6	2.8	2158	21	AAAF16153	Human prostate can
18	49.8	2.6	6644	20	AAAX3181	Base sequence of t
19	49.8	2.6	7372	20	AAAX3182	Base sequence of t
20	49.8	2.6	7797	20	AAAX3180	Cowpox virus bsr f
21	49.8	2.6	7996	20	AAH33184	Base sequence of t
22	49.6	2.6	4590	22	AAH24065	Yeast AOD9604-asso
23	49.4	2.6	244	22	AAAF58238	Oligonucleotide D1
24	49.2	2.6	244	22	AAAF58238	Oligonucleotide D1
25	48.6	2.5	2338	15	AAO54656	Plasmid pNX1 comp
26	48	2.5	240	18	AAAT76782	Staphylococcus aur
27	48	2.5	2195	21	AAAI4072	Human SPROUTY-1 pa
28	48	2.5	2364	21	AAZ33323	Human secreted pro
29	47.2	2.5	1020	21	AAZ97182	Human prostate can
30	47.2	2.5	3375	20	AAZ07192	Human lung tumour
31	47.2	2.5	3275	21	AAAC79145	Human lung tumour
32	47	2.5	2921	21	AAAC77829	Human cancer assoc
33	46.8	2.5	268	22	AAH70080	Human cervical can
34	46.8	2.5	2057	22	AAAF72803	Secreted protein g
35	46.4	2.5	1117	21	AAAS9475	Nucleotide sequenc
36	46.4	2.5	3060	22	AAO02924	Human PRO5723 cDNA
37	46.4	2.5	3060	22	AAAF44263	Human PRO5723 nucl
38	46.4	2.5	3060	22	AAAC91489	Human PRO5723 cDNA
39	46.2	2.4	1582	17	AAAT28259	Survival motor neu
40	46.2	2.4	1582	17	AAAT1831	Human survival mot
41	46	2.4	464	22	AAH33241	Human colon cancer
42	46	2.4	1119	21	AAAC60033	Human secreted pro
43	46	2.4	1492	21	AAAC98102	Human colon cancer
44	46	2.4	1493	22	AAH34433	Human colon cancer
45	46	2.4	2475	21	AAAT77667	Human PRO1246 cDNA

ALIGNMENTS

RESULT 1	
AAC41897	
ID AAC41897 standard; DNA: 1164 BP.	
AC AAC41897;	
XX	
DT 17-OCT-2000 (first entry)	
XX	
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 33540.	
XX	
KW Hybridisation assay; genetic mapping; gene expression control;	
KW protein identification; signal transduction pathway;	
KW metabolic pathway; promoter; termination sequence; ss.	
XX	
OS Arabidopsis thaliana.	
XX	
PN EP1033405-A2.	
XX	
PD 06-SEP-2000.	
XX	
PF 25-FEB-2000; 2000EP-0301439.	
XX	
PR 25-FEB-1999; 99US-0121825.	
PR 05-MAR-1999; 99US-0123180.	
PR 09-MAR-1999; 99US-0123548.	
PR 23-MAR-1999; 99US-0125788.	
PR 25-MAR-1999; 99US-0126264.	
PR 29-MAR-1999; 99US-0126785.	
PR 01-APR-1999; 99US-0127462.	
PR 06-APR-1999; 99US-0128234.	
PR 08-APR-1999; 99US-0128714.	
PR 16-APR-1999; 99US-0129845.	
PR 19-APR-1999; 99US-0130077.	
PR 21-APR-1999; 99US-0130449.	

PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-01332484.
PR 05-MAY-1999; 99US-01332485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135253.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140354.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.

PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145224.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 28-JUL-1999; 99US-0145919.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149358.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.

[illegible]

Query Match	8.4%	Score 158.2	DB 21	Length 446
Best Local Similarity	74.5%	Pred. No. 6.4e-30		
Matches 199	Conservative	0	Mismatches 66	Indels 0
			Gaps	0

OY	788	ggctatggccatggaacacctctcttccaaatgctccaggaatgatgatgaacggtgtc	847
Db	1	ggcaatgcacatggaatcgcgtgcctctccaaacttccgatacagtgatgaaatgatg	60
OY	848	gaccacaatgtttctgacacatagacgaattcggctggaattctgataattgtttacatcgc	907
Db	61	gagcaaatgcctttccaagaataagcagttgtgtgtcgtcttaccctagttactgttc	120
OY	908	catcatatcgttttgcgttgagttgattatrtttgagtcacagagaagcttcacgaat	967
Db	121	aataatctctgtaacgycggaggtcttggaatactggaagcagagagctgcacgaat	180
OY	968	taagcctctctataagatcatlcatcagccaccatatactacaacaagacgaatacaat	1027
Db	181	taaacocctttacaagatcctcacatgacgaacaatcacatctacaataagcagacacact	240
OY	1028	ctctccattgycggttaagtcttca	1054
Db	241	ttctccctttgycggttcggttca	267

RESULT 4
 AAF58252/C
 ID AAF58252 standard; DNA: 936 BP.
 XX
 AC AAF58252;
 XX
 DT 24-APR-2001 (first entry)
 XX
 DE Oligonucleotide D1835.
 XX
 KW Electron-transfer group; ETM: mismatch; genotyping;
 KM gene expression, ss.
 XX
 OS Synthetic.
 OS
 PN WO200107665-A2.
 XX
 PD 01-FEB-2001.
 XX
 PF 26-JUL-2000; 2000WO-US20476.
 XX
 PR 26-JUL-1999; 9905-0145695.
 PR 17-MAR-2000; 2000US-0190259.
 XX
 PA (CLIN-) CLINICAL MICRO SENSORS INC.
 XX
 PI umek RM;
 XX
 DR WPI: 2001-159728/16.
 XX
 PT Nucleic acids containing electron-transfer group, useful as labels in
 PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
 PT a single surface -
 PS
 PS Example 6: Page 127; 159pp; English.
 CC
 CC The present invention relates to a composition comprising two nucleic
 CC acids each containing an electron-transfer group (ETM) having
 CC different redox potentials. The invention is used for electronic
 CC detection of nucleic acids, especially of substitutions (mismatches)
 CC and single-nucleotide polymorphisms, e.g. for genotyping,
 CC monitoring gene expression.
 XX
 SO Sequence 936 BP: 4 A; 139 C; 10 G; 7 T; 776 other;

Query Match	7.18; Score 134.6; DB 22; Length 936;
Best Local Similarity	0.68; Pred. No. 6,1e-24;
Matches	5; Conservative 498; Mismatches 282; Indels 0; Gaps 0


```
QY 988 tcatgccaccatcatactacaagaagaaatcacctctccattgcggtagt 1047
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 185 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 126
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1048 gtttcagttgtctctcttcttctgtctgttaagaattgtagcatttcttca 1107
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 125 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 66
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1108 gaaagaactgttcagaagctgtctgtactccaatacacattgtccttaccata 1167
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 65 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 6
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1168 aagta 1172
      : : : :
Db 5 wwwwww 1

RESULT 6
AAFS8257/c
ID AAF58257 standard; DNA; 936 BP.
XX
AC AAF58257;
XX
DT 24-APR-2001 (first entry)
XX
DE Oligonucleotide D1954.
XX
KM Electron-transfer group; ETM; mismatch; genotyping;
KM gene expression; ss.
XX
OS Synthetic.
XX
PN WO200107665-A2.
XX
PD 01-FEB-2001.
XX
PF 26-JUL-2000; 2000MO-US20476.
XX
PR 26-JUL-1999; 9905-0145695.
XX
PR 17-MAR-2000; 2000US-0190259.
XX
PA (CLIN-) CLINICAL MICRO SENSORS INC.
XX
PI Umek RM;
XX
DR WPI; 2001-159728/16.
XX
XX Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface.
XX
XX Example 6; Page 127; 159pp; English.
XX
XX The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
XX Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;
SQ

Query Match 7.1%; Score 134.6; DB 22; Length 936;
Best Local Similarity 0.6%; Pred. No. 6.1e-24;
Matches 5; Conservative 498; Mismatches 282; Indels 0; Gaps 0;
```

```
Db 725 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 666
QY 508 atattgtgcatactccataaggaattgaacagttagtgctatataagtttc 567
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 665 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 606
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 568 gtgaacccaatgagaagtcgtacacttgaagttgaatttctacttgccattaaagtc 627
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 605 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 546
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 628 cacttaaatgttgtgaagtgatgtctcaacttcagacaactctttctgctctc 687
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 545 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 486
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 688 tgagactcgtcttgaatcttcttctgtctgttcttgcctgaatgaactccta 747
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 485 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 426
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 748 caataaagctatgcgttttgcaaatgttgcgaatgaagctatgcattgacacac 807
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Db 425 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 366
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 808 ttctccaactgtctccgagagctatgtatgaagtggttgaccacaattgttgcagca 867
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 365 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 306
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 868 tagacgaattcgcgtgattctgtattgtttacatcgcacatcattgttctgtg 927
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 305 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 246
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 928 agtttgatattatgtatgcacagagacttcataagcctcctcblataagtc 987
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 245 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 186
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 988 tcatgccaccatcatactacaagaagaatacacctctccattgcggtagt 1047
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 185 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 126
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1048 gtttcagttgtctctcttcttctgtctgttaagaattgtagcatttcttca 1107
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 125 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 66
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1108 gaaagaactgttcagaagctgtctgtactccaatacacattgtccttaccata 1167
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 65 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 6
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1168 aagta 1172
      : : : :
Db 5 wwwwww 1

RESULT 7
AAFS8259/c
ID AAF58259 standard; DNA; 936 BP.
XX
AC AAF58259;
XX
DT 24-APR-2001 (first entry)
XX
DE Oligonucleotide D2004.
XX
XX Electron-transfer group; ETM; mismatch; genotyping;
KM gene expression; ss.
XX
XX Synthetic.
XX
PN WO200107665-A2.
XX
PD 01-FEB-2001.
XX
PF 26-JUL-2000; 2000MO-US20476.
XX
PR 26-JUL-1999; 9905-0145695.
```


Oy	568	gtgcaacaaagaagaaatcgtaactcttggaattgaatttctcactgcattaagtcc	627
Db	605	wwwwwmmmw	546
Oy	628	cacttaaatttgtttgtaaggtagttgtcacttcacaacatacttcttcgtctccc	687
Db	545	mmw	486
Oy	668	tgaagactgtcctaagtcttbaaaccttlttggctgtlcttcctcagaatgcattccta	747
Db	485	wwwwwmmmw	426
Oy	748	caataaaggcatgcgtcttgcaaatgtttgqcaa tgaagcata gcatggtacactc	807
Db	425	wwwwwmmmw	366
Oy	808	tcttccaacctgtctccagagatgatlgaaacgttggttgaccaaatgttttgctaaga	867
Db	365	mmw	306
Oy	868	tagcacgaatcgcgtcgatcctgtattgttttacaccgcacatcattgtttcgltg	927
Db	305	wwwwwmmmw	246
Oy	928	agtttgatttatctgatgcacagagatcattacatatgaacctcctaagtacc	987
Db	245	wwwwwmmmw	186
Oy	988	tccatgcacccaalatalactacaacagacagatacactctctcaattgcgylaat	1047
Db	185	wwwwwmmmw	126
Oy	1048	gtttcagttgtctctcttagttcttcttgaaaagatigtgacattagtttcttacc	1107
Db	125	wwwwwmmmw	66
Oy	1108	gaaaagacttbtgcagacgtctgttactccaatcacatttgoatlccctatcacata	1167
Db	65	mmw	6
Oy	1168	aagta 1172	
Db	5	mmmmw 1	
RESULT_9			
ID	AAF58255/c		
AC	AAF58255 standard; DNA; 938 BP.		
XX	AAF58255;		
DT	24-APR-2001 (first entry)		
DE	Oligonucleotide D1876.		
KW	Electron-transfer group; ETM; mismatch; genotyping:		
OS	Synthetic.		
PX	MO200107665-A2.		
PN	01-FEB-2001.		
PD	26-JUL-2000; 2000MD-US20476.		
PF	26-JUL-1999; 99US-0145695.		
PR	17-MAR-2000; 2000US-0190259.		
RA	(CLIN-) CLINICAL MICRO SENSORS INC.		
PL	Umek RM;		

[illegible]

```
Db 65 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 6
Qy 1168 aagta 1172
    : : : :
Db 5 wwwwww 1

RESULT 10
AAF58252
ID AAF58252 standard; DNA; 936 BP.
XX
AC AAF58252;
XX
DT 24-APR-2001 (first entry)
XX
DE Oligonucleotide D1875.
XX
KW Electron-transfer group; ETM; mismatch; genotyping;
    gene expression; ss.
XX
OS Synthetic.
XX
PN WO200107665-A2.
XX
PD 01-FEB-2001.
XX
PE 26-JUL-2000; 2000MO-US20476.
XX
PR 26-JUL-1999; 99US-0145695.
PR 17-MAR-2000; 2000US-0190259.
XX
PA (CLIN-) CLINICAL MICRO SENSORS INC.
XX
PI Umek RM;
XX
DR WPI; 2001-159728/16.
XX
PT Nucleic acids containing electron-transfer group, useful as labels in
    hybridization assays, e.g. for genotyping, allowing repeat analyses on
    a single surface
XX
PS Example 6; Page 127; 159pp; English.
XX
CC The present invention relates to a composition comprising two nucleic
    acids each containing an electron-transfer group (ETM) having
    different redox potentials. The invention is used for electronic
    detection of nucleic acids, especially of substitutions (mismatches)
    and single-nucleotide polymorphisms, e.g. for genotyping,
    monitoring gene expression.
CC
XX
SQ Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other:

Query Match 7.1%; Score 133.8; DB 22; Length 936;
Best Local Similarity 0.8%; Pred. No. 9,7e-24;
Matches 6; Conservative 493; Mismatches 280; Indels 0; Gaps 0:

Qy 326 ttctacatcttacccttaaaatcaagcttaacctcccaagaagtcgcgaacttcaactt 385
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 3 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 62
Qy 386 tgtatcacatcttgcttaagcttcctcatgltatcgattttcaatttaagggaagagg 445
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 63 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 122
Qy 446 ttcttcgtgactgtaacagtaattggaattgtagtgatgtagtcacgttgcattat 505
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 123 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 182
Qy 506 tgaatatttgacatactccatcaactaaggagatgaacagtgtagtgcttatataagtt 565
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 183 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 242
```

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Qy 566 ttgtcaaccaatgagaagctgacatcttgaagttgaatttctacttgcaattaa 625
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 243 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 302
Qy 626 tccacttaaatgttgtgaagtgatgctacttcaacacatcttcttgccttc 685
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 303 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 362
Qy 686 tctgagactcgtcttaattgaaacttttttgctcgttttgcttaaatgcaatcc 745
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 363 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 422
Qy 746 tacaataaagctatgcttgcaaatgttgtgcaatgaagctatgcatgtlacac 805
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 423 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 482
Qy 806 tcttcccaactgctccgagatgataatgaacgttgtgaccaa:gtttgctag 865
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 483 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 542
Qy 866 cataagcaatcgagctgatactgtattgtttacatgcacatctat:ttgtttcgt 925
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 543 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 602
Qy 926 tgaagtttgattatlgatgacagagagcttcaatgaagcttctataagta 985
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 603 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 662
Qy 986 tctcatgcccacccatcatctacaacaagacagatacactctccattgcccgtaa 1045
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 663 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 722
Qy 1046 gtgtttcaagttgtctctctttagtctctgttaaagattgtagcaattgttctcta 1104
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 723 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 781

RESULT 11
AAF58254
ID AAF58254 standard; DNA; 936 BP.
XX
AC AAF58254;
XX
DT 24-APR-2001 (first entry)
XX
DE Oligonucleotide D1875.
XX
KW Electron-transfer group; ETM; mismatch; genotyping;
    gene expression; ss.
XX
OS Synthetic.
XX
PN WO200107665-A2.
XX
PD 01-FEB-2001.
XX
PE 26-JUL-2000; 2000MO-US20476.
XX
PR 26-JUL-1999; 99US-0145695.
PR 17-MAR-2000; 2000US-0190259.
XX
PA (CLIN-) CLINICAL MICRO SENSORS INC.
XX
PI Umek RM;
XX
DR WPI; 2001-159728/16.
XX
PT Nucleic acids containing electron-transfer group, useful as labels in
    hybridization assays, e.g. for genotyping, allowing repeat analyses on
    a single surface
XX
PS Example 6; Page 127; 159pp; English.
XX
```

CC The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.

50 Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;

Query Match	7.18	Score	133.8	DB	22	Length	936
Best Local	Similarity	0.88	Pred. No.	9.7e-24			
Matches	6	Conservative	493	Mismatches	280	Indels	0
						Gaps	0

OY	326	tttaacatctattacctaataacagtttactctccaaagttcgcgcttcactt	385
Dp	3	62
OY	386	tgatattcactatctgcttaatcgcctctctatctatctgaatttccaatttaaggaagag	445
Dp	63	122
OY	446	tttctctgctgacgttacagataatttggaatttgatctgtagagttcaagtttcgaattat	505
Dp	123	182
OY	506	tgatatttgtagcatattctccatctcaagagatgtgaacagtttagtgcctatataagttc	565
Dp	183	242
OY	566	ttgtgcaaccaaataagaaagtcgtatcatcttcttgaagtgaatttctactgcatttaag	625
Dp	243	302
OY	626	tccacttaaatgttctgttagagtgatgctctacttcagaacacatctttctcgtctc	685
Dp	303	362
OY	686	tcctgagactcgtccttagtttgaaatccttttggctcgtgttcttgcttcgaatgaattcc	745
Dp	363	422
OY	746	tacaaataaaggcatctgcgtttgcaaatcgttctgtgcaatgaagcctatgcacatggtacac	805
Dp	423	482
OY	806	tcttctccaaacgtctcccgagatgatgtgaacgtgttggaaccaatggtttgctag	865
Dp	483	542
OY	866	catagagcaatctggcgtgagatctcgtatatttgtttaacatcgccatctatctgtttcgt	925
Dp	543	602
OY	926	tgagtttgtagtattatctgtagatgcacagagcttcacatgaattgaagcctctcataagta	985
Dp	603	662
OY	986	tctccatgcccacacatcatctacaacaaagcagaatatacatctctccatttgcggttaa	1041
Dp	663	722
OY	1046	gtgttttcaagtttctctctcttgcttgcttgtaaaaagatggtgacattagtttctta	1104
Dp	723	781

RESULT	12
AAF58257	
ID	AAF58257 standard; DNA; 936 BP.
XX	
AC	AAF58257;
XX	

```

DT 24-APR-2001      (first entry)
DE Oligonucleotide D1954.
KW Electron-transfer group; ETM; mismatch; genotyping;
   gene expression; ss.
OS Synthetic.
PN WO200107665-AZ.
PD 01-FEB-2001.
XX
XX
XX 26-JUL-2000; 2000WO-US20476.
PF
PR 26-JUL-1999;    99US-0145695.
   17-MAR-2000; 2000US-0190259.
XX
XX (CLIN-) CLINICAL MICRO SENSORS INC.
PA
PI Umek RM;
PT WPI: 2001-159728/16.
DR
XX Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PR a single surface _
PS Example 6; Page 127; 159pp; English.
XX
XX The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
CC
SQ Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;

Query Match          7.1%; Score 133.8; DB 22; Length 936;
Best Local Similarity 0.8%; Pred. No. 9,7e-24;
Matches    6; Conservative 493; Mismatches 280; Indels    0; Gaps    0;

QY 326 ttctcaatcattacttaactaaacgaagtcctcccaagaagctcgacttcaactt 385
DB   : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
   3 www..... 62

QY 386 tgcataccaalgtctaatacgcttctcatalcatgatlccaatttaaaggaaagg 445
DB   : ::::: ::::: *:::: ::::: ::::: |:::: ::::: ::::: :::::
   63 www..... 122

QY 446 ttcttcgtgacgcgtacagtaatttgatgtgatgtagtcatglttgcatatt 505
DB   : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
   123 www..... 182

QY 506 tgattatttgtcatatccatccataaaggagttgaacagttagtgcttatataagtt 565
DB   : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
   183 www..... 242

QY 566 ttgtgcacaacaaatggaaagtcgtacatctlttgaattgaatttctacttgcattaa 625
DB   : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: |::::
   243 www..... 302

QY 626 tccaacttaaatgttgttgaagtgatgctcaacttcaagacaatcttctcgtctc 685
DB   : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
   303 www..... 362

QY 686 tcctggacctcgtcttaagtttgaatccttcttgcctcgttttgctccaagtcatcc 745
DB   : ::::: ::::: ::::: ::::: || ::::: ::::: ::::: :::::
   363 www..... 422

QY 746 taacaataaagcgtacacgcttgcacaatttttgtgcataaaggatcacatgtacac 805

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Query Match	7.1%	Score 133.8;	DB 22;	length 936;
Best Local Similarity	0.88;	Pred. No. 9.7e-24;		
Matches	6;	Conservative 493;	Mismatches 280;	Indels 0;
				Gaps 0;

[illegible]

[illegible]

XX	RESULT 13
XX	AAF58259
ID	AAF58259 standard; DNA; 936 BP.
AC	AAF58259;
XX	
DT	24-APR-2001 (first entry)
XX	
DE	Oligonucleotide D2004.
XX	
KW	Electron-transfer group; ETM; mismatch; genotyping;
KW	gene expression; ss.
XX	
OS	Synthetic.
XX	
PN	WO200107665-A2.
XX	
PD	01-FEB-2001.
XX	
PE	26-JUL-2000; 2000WO-US20476.
XX	
PR	26-JUL-1999; 99US-0145695.
PR	17-MAR-2000; 2000US-0190259.
XX	
PA	(CLIN-) CLINICAL MICRO SENSORS INC.
XX	
P1	Umek BM;
XX	
DR	WPI; 2001-159728/16.
XX	
PT	Nucleic acids containing electron-transfer group, useful as labels in
PT	hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT	a single surface -
XX	
PS	Example 6; Page 128; 159pp; English.
XX	
XX	The present invention relates to a composition comprising two nucleic
CC	acids each containing an electron-transfer group (ETM) having
CC	different redox potentials. The invention is used for electronic
CC	detection of nucleic acids, especially of substitutions (mismatches)
CC	and single-nucleotide polymorphisms, e.g. for genotyping,
CC	monitoring gene expression.
XX	
XX	Sequence 936 BP; 6 A; 138 C; 8 G; 8 T; 776 other;

Query Match 7.1%; Score 133.8; DB 22; Length 936;
 Best Local Similarity 0.8%; Pred. No. 9.7e-24;
 Matches 6; Conservative 493; Mismatches 280; Indels 0; Gaps 0

[illegible]

RESULT 14	
AAFS8262	
ID	AAFS8262 standard; DNA; 936 BP.
XX	
AC	AAFS8262;
XX	
DT	24-APR-2001 (first entry)
XX	
DE	Oligonucleotide D2007.
XX	
KW	Electron-transfer group; ETM; mismatch; genotyping;
KW	gene expression; ss.
XX	
OS	Synthetic.
XX	
PN	WO200107665-A2.
XX	
PD	01-FEB-2001.
XX	

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```
Db 61 CFYIYLLKINVLKPKDAITIKAMRLQMFVANKAMPWYLLPTVSSMERGWTGCFASI 120
OY 121 DEFGWILYFVYIAYLVFEFGIYWMHRELHDIKPLKYKTLHATHTHYNKNTLSPFAGLA 180
Db 121 DEFGWILYFVYIAYLVFEFGIYWMHRELHDIKPLKYKTLHATHTHYNKNTLSPFAGLA 180
OY 181 FHPVDGIILOAVPHVIALFTVPIHFTTHIGLLFMEAIWTANIHDCIHGNTIPVWAGAGYHTI 240
Db 181 FHPVDGIILOAVPHVIALFTVPIHFTTHIGLLFMEAIWTANIHDCIHGNTIPVWAGAGYHTI 240
OY 241 HHTTYKHNKGHTYIMDMWFGSLRDLPLEDDNKDSFKKAE 281
Db 241 HHTTYKHNKGHTYIMDMWFGSLRDLPLEDDNKDSFKKAE 281

RESULT 2
O9SYS2 PRELIMINARY: PRT: 281 AA.
AC 09SYS2:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE STEROL-C5-DESATURASE.
CN F16B3.21.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA; TISSUE=LEAVES;
RX MEDLINE=99273992; PubMed=10344195;
RA Huseinstein T., Schaller H., Gachotte D., Benveniste P.;
RT "Delta-sterol-C5-desaturase:molecular characterization and functional
expression of wild-type and mutant alleles.";
RL Plant Mol. Biol. 39:891-906(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X., Kaul S., Town C.D., Benito M., Greasy T.H., Haas B., Wu D.,
Roning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
R Bowan C.L., White O., Fujii C.Y., Fraser K.M.;
RT "Arabidopsis thaliana chromosome III BAC F16B3 genomic sequence.";
RX Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF069468; AAD12944.1; -.
DR EMBL; AC021640; AAF32465.1; -.
DR InterPro: IPR001541; Sterol_desat.
DR Pfam: PF01598; Sterol_desat.1.
SQ SEQUENCE 281 AA: 33142 MW: D32B1BCDC467D7 CRC64;
```

```
Db 241 HHTTYKHNKGHTYIMDMWFGSLRDLPLEDDNKDSFKKAE 281
|||||
RESULT 3
O9SYS2 PRELIMINARY: PRT: 281 AA.
AC 09SYS2:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE STEROL-C5-DESATURASE.
CN F16B3.22.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA; TISSUE=LEAVES;
RX MEDLINE=97077348; PubMed=8919915;
RA Gachotte D., Huseinstein T., Bard M., Lacroste F., Benveniste P.;
RT "Isolation and characterization of an Arabidopsis thaliana cDNA
encoding a delta 7-sterol-C5-desaturase by functional complementation
of a defective yeast mutant.";
RL Plant J. 9:391-398(1996).
DR EMBL; X90454; CAA62079.1; -.
DR EMBL; 12510; Atath.1710;12510.
DR InterPro: IPR001541; Sterol_desat.
DR Pfam: PF01598; Sterol_desat.1.
SQ SEQUENCE 281 AA: 33121 MW: 84C7E6167D2974B7 CRC64;
```

Query Match 98.5%; Score 1538; DB 10; Length 281;
Best Local Similarity 98.6%; Pred. No. 3.4e-126;
Matches 277; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
OY 1 MAADNAYLMQFVDETSFYRIYLSHLLPANLWEPRLPHLQTLWLRNLAAGTLLYISGFILM 60
Db 1 MAADNAYLMQFVDETSFYRIYLSHLLPANLWEPRLPHLQTLWLRNLAAGTLLYISGFILM 60
OY 61 CFYIYLLKINVLKPKDAITIKAMRLQMFVANKAMPWYLLPTVSSMERGWTGCFASI 120
Db 61 CFYIYLLKINVLKPKDAITIKAMRLQMFVANKAMPWYLLPTVSSMERGWTGCFASI 120
OY 121 DEFGWILYFVYIAYLVFEFGIYWMHRELHDIKPLKYKTLHATHTHYNKNTLSPFAGLA 180
Db 121 DEFGWILYFVYIAYLVFEFGIYWMHRELHDIKPLKYKTLHATHTHYNKNTLSPFAGLA 180
OY 181 FHPVDGIILOAVPHVIALFTVPIHFTTHIGLLFMEAIWTANIHDCIHGNTIPVWAGAGYHTI 240
Db 181 FHPVDGIILOAVPHVIALFTVPIHFTTHIGLLFMEAIWTANIHDCIHGNTIPVWAGAGYHTI 240
OY 241 HHTTYKHNKGHTYIMDMWFGSLRDLPLEDDNKDSFKKAE 281
Db 241 HHTTYKHNKGHTYIMDMWFGSLRDLPLEDDNKDSFKKAE 281

RESULT 4
O9SYS2 PRELIMINARY: PRT: 279 AA.
AC 09SYS2:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PUTATIVE STEROL-C5-DESATURASE.
CN F16B3.22.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
```

RC STRAIN-CV, COLUMBIA;
 3A Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
 3B Rongling C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
 3C Bowman C.L., White O., Niernan W.C., Fraser C.M.,
 3T "Arabidopsis thaliana chromosome III BAC F1683 genomic sequence."
 3L Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC021640; AAF32466.1;
 DR InterPro: IPR001541; Sterol_desat.
 DR Pfam: PF01598; Sterol_desat; 1.
 SQ SEQUENCE 279 AA; 33111 MW; DCAB107445FA2795 CRC64;

Query Match 81.0%; Score 1265.5; DB 10; Length 279;
 Best Local Similarity 79.4%; Pred. No. 1.7e-102;
 Matches 224; Conservative 26; Mismatches 27; Indels 5; Gaps 2;

QY 1 MAADNA-YLMQFVDETSFYNRIVLSHLPLANLMEPLPHFLOTWLRNYLAGTLLYFISGFL 59
 DB 1 MAATMADYNQDIVNETSFYNRIVLSHLPLANLMEPLPHFLOTWLRNYLAGTLLYFISGFL 60
 QY 60 WCFEYIYKINIVYLPKAIPTIKAMRLQMFVAMKAMPYTLPTVSESMIERGWTCKFAS 119
 DB 61 WCFEYIYKINIVYLPKAIPTIKAMRLQMFVAMKAMPYTLPTVSESMIERGWTCKFAS 120
 QY 120 IDEFGWILYEVYIAIVLVEFEGIYMMHRELHDIKPLKYLAATHNHYNKNQNTLSPFAGL 179
 DB 121 LDHNMFLCFIYALYLVEFMILYVWKEHDIKFLYKHLATHNHYNKNQNTLSPFAGL 180
 QY 180 AFHPVDGILQAVPHVIALFPIPIHTTHIGLLEMEAIWTANIHDCIHGNIWPMVAGAYHT 239
 DB 181 AFHPLDGLQAIPIHVIALFPIPIHILTHLSLPLEGIWTASIHDCIHGNIWPMVAGAYHT 240
 QY 240 IHHTYKHNHGYTIWMDMFGSLRDLPLEDDKDKSKFAE 281
 DB 241 IHHTYKHNHGYTIWMDMFGSLRDLPLEDDKDKSKFAE 282

RESULT 5
 092729 PRELIMINARY; PRT; 271 AA.
 AC 092729;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE SPEROI-C5(6)-DESATURASE.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
 NX NCBI_TaxID=4097;
 RX
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV, XANTHI SH6; TISSUE-CALLI DERIVED FROM LEAF PROTOPLASTS;
 RA Husselstein T., Schaller H., Gachotte D., Benveniste P.;
 RT "Sterol-C5(6)-desaturase: molecular characterization and functional
 expression of wild-type and mutant alleles."
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF081194; AAD04034.1;
 DR Mendel: 36287; Nica: 1710; 36287.
 DR InterPro: IPR001541; Sterol_desat.
 DR Pfam: PF01598; Sterol_desat; 1.
 SQ SEQUENCE 271 AA; 31842 MW; 361520EAAB5686F CRC64;

Query Match 76.8%; Score 1199.5; DB 10; Length 271;
 Best Local Similarity 77.2%; Pred. No. 9.2e-97;
 Matches 207; Conservative 27; Mismatches 33; Indels 1; Gaps 1;

QY 7 YLMQFVDETSFYNRIVLSHLPLANLMEPLPHFLOTWLRNYLAGTLLYFISGFLMCFYIY 66
 DB 4 YLMQFVDETSFYNRIVLSHLPLANLMEPLPHFLOTWLRNYLAGTLLYFISGFLMCFYIY 63
 QY 67 LKINIVLPKAIPTIKAMRLQMFVAMKAMPYTLPTVSESMIERGWTCKFASIDEFGMI 126

DB 64 LKRNVIYKDAIPSKAMRLQMFVAMKAMPYTLPTVSESMIERGWTCKFASIDEFGMI 123
 QY 127 LYEVYIYLVFEFGIYMMHRELHDIKPLKYLAATHNHYNKNQNTLSPFAGLAFHPVDG 186
 DB 124 SVYIAAYLYLVFEFGIYMMHRELHDIKPLKYLAATHNHYNKNQNTLSPFAGLAFHPVDG 183
 QY 187 ILQAVPHVIALFPIPIHTTHIGLLEMEAIWTANIHDCIHGNIWPMVAGAYHTIHTTYK 246
 DB 184 ILQAVPHVIALFPIPIHTTHIGLLEMEAIWTANIHDCIHGNIWPMVAGAYHTIHTTYK 243
 QY 247 HNYGHYTIWMDMFGSLRDLPLEDDK 274
 DB 244 HNYGHYTIWMDMFGSLRDLPLEDDK 270

RESULT 6
 09XE12 PRELIMINARY; PRT; 271 AA.
 AC 09XE12;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE STEROL-C5(6)-DESATURASE HOMOLOG.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
 NX NCBI_TaxID=4097;
 RX
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV, XANTHI SH6; TISSUE-LEAF;
 RA Husselstein T., Schaller H., Gachotte D., Benveniste P.;
 RT "Delta7-sterol-C5-desaturase: molecular characterization and
 functional expression of wild-type and mutant alleles."
 RL Plant Mol. Biol. 39:891-906(1999).
 DR EMBL: AF099669; AAD04058.1;
 DR InterPro: IPR001541; Sterol_desat.
 DR Pfam: PF01598; Sterol_desat; 1.
 SQ SEQUENCE 271 AA; 32036 MW; 1E705A0B69C320D4 CRC64;

Query Match 74.6%; Score 1165; DB 10; Length 271;
 Best Local Similarity 75.8%; Pred. No. 9.3e-94;
 Matches 200; Conservative 29; Mismatches 35; Indels 0; Gaps 0;

QY 7 YLMQFVDETSFYNRIVLSHLPLANLMEPLPHFLOTWLRNYLAGTLLYFISGFLMCFYIY 66
 DB 4 YLMQFVDETSFYNRIVLSHLPLANLMEPLPHFLOTWLRNYLAGTLLYFISGFLMCFYIY 63
 QY 67 LKINIVLPKAIPTIKAMRLQMFVAMKAMPYTLPTVSESMIERGWTCKFASIDEFGMI 126
 DB 64 LKRNVIYKDAIPSKAMRLQMFVAMKAMPYTLPTVSESMIERGWTCKFASIDEFGMI 123
 QY 127 LYEVYIYLVFEFGIYMMHRELHDIKPLKYLAATHNHYNKNQNTLSPFAGLAFHPVDG 186
 DB 124 SVYIAAYLYLVFEFGIYMMHRELHDIKPLKYLAATHNHYNKNQNTLSPFAGLAFHPVDG 183
 QY 187 ILQAVPHVIALFPIPIHTTHIGLLEMEAIWTANIHDCIHGNIWPMVAGAYHTIHTTYK 246
 DB 184 ILQAVPHVIALFPIPIHTTHIGLLEMEAIWTANIHDCIHGNIWPMVAGAYHTIHTTYK 243
 QY 247 HNYGHYTIWMDMFGSLRDLPLEDDK 270
 DB 244 HNYGHYTIWMDMFGSLRDLPLEDDK 267

RESULT 7
 09E0S5 PRELIMINARY; PRT; 299 AA.
 AC 09E0S5;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)

RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA Toriumi M., Vaysberg M., Yu G., Federitz J., N.A., Theologis A.,
RA Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC F2265 from chromosome
I.";
RN Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RL
RN [2]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RL
RN [3]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RL
RN [4]
RP SEQUENCE FROM N.A.
RA Cheuk R., Shin P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA Khan S., Kim C., Altafi H., Bel B., Chin C., Chlou J., Choi E.,
RA Com L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federitz J.,
RA Theologis A., Ecker J.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC022464; AAF79571.1; -;
DR InterPro: IPR001541; Sterol_desat.
DR Pfam: PF01598; Sterol_desat; 1.
SQ SEQUENCE 261 AA; 30493 MW; 83DBE0A795CC749F CRC64;

Query Match 11.3%; Score 176; DB 10; Length 261;
Best Local Similarity 22.6%; Pred. No. 9.8e-08;
Matches 65; Conservative 33; Mismatches 77; Indels 112; Gaps 14;
QY 42 WLRNYLA-----GTL-----YFISGFLMCF----- 62
DB 2 WLMQYLVTHFSDFQLACISGFLHESVFLSGLPFTLEKOGFLSKYKIGTKNNTPAAG 61
QY 63 -----YIYVLYKINVLPRKDIPTIKAMRLQMFVAMKAMPWYTLPTVSESMTERGWTKC 116
DB 62 KCTIRLLVHFVSNPLRLMLASVPFRAMGR-----SSPF-----LPS-----WKVEY 103
QY 117 FASIDFGMLRVYVYAIYLVFVEGCIYMMHRELHDKPLRYKLATPHIYKNTLSPP 176
DB 104 SAQ-----ILFFIIEDFVFWGCHRIHS-KWLYKNVSHVNHYY-----ATPR 145
QY 177 A-----GLAFHRYDGLIQAIVPHYIALFIVPHIHTTHIGLFPMAITANIHDC 224
DB 146 GLTSEYAHNAEILFLGFATVIGPALTGPHILITLWL-----WVLAVLETVANHC 195
QY 225 IH-----GNIMPVV-GAGYHTTINT--TYKNVYGHTTMMDMFGS 262
DB 196 YHRPWSLNFRLPLYGADPFHDYHNRLLYTKSGNYSFVYMDMIFCG 242
RESULT 13
Q20612 PRELIMINARY; PRT; 286 AA.
AC Q20612;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE F49E12.10 PROTEIN.
GN F49E12.10.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Felodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Thomas K.;
RT Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.

RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsy T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA Smaildon N., Smith A., sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
RL Nature 368:32-38(1994).
DR EMBL: Z66520; CAA91384.1; -;
DR InterPro: IPR001541; Sterol_desat.
DR Pfam: PF01598; Sterol_desat; 1.
SQ SEQUENCE 286 AA; 33874 MW; EA9A7468A98D8817 CRC64;

Query Match 11.2%; Score 174.5; DB 5; Length 286;
Best Local Similarity 22.4%; Pred. No. 1.5e-07;
Matches 64; Conservative 49; Mismatches 112; Indels 61; Gaps 14;
QY 39 LQWLRNYLAGT--LLYFTSG-----FLMCEYIYVLYKINVLPRKDIPTIKAMRLQMFV 90
DB 5 LYRLVNYFGDGEYMLYVYVGNVAGISFMYLNLFFIIIDVDPK----WVQYKIQEEK 60
QY 91 AMKAMPWYTLPTVSES-----IERGTCFASIDFGMLRVYVYAIYV 137
DB 61 KPSLSYVLSLTKVGNOLIVPIVITLWYVAVRMGMFGVPVIP-SWYILRLDACLMA 119
QY 138 FVEGCIYMMHRELHDKPLRYKLHATHNIYKNTLSPPFAGLAFHRYDGLIQAIVPHYAL 197
DB 120 MEDIGFYTHRLFNPK-LYKHINKKHENKAVSIS--SIANLE--NAISLSPI 172
QY 198 FIVPHIHTTHI--GLFMEAITANIHDCIGNIMPVV-GAGYHTTINTTYKNYGHYT 253
DB 173 YLCAVLFRCHVVSHTYLSAIIITTFHH--SGYHPRFMLSABHNDHFNHKVFECYGCGR 230
QY 254 IYMDMFG-----SLRDP-----LLEEDDKDSFK 279
DB 231 --LDWLHGDTFRKSIENHRDYVYVYGTPIKELIPEDKNNNNK 274
RESULT 14
Q90010 PRELIMINARY; PRT; 115 AA.
AC Q90010;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE HYPOTHEICAL PROTEIN (FRAGMENT).
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=968 H90.
RA Ding D.;
RT "Generation and analysis of GFP-gene fusion library of fission
yeast.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB027881; BAA87185.1; -;
DR InterPro: IPR001541; Sterol_desat.
FT NON_TER 1 115
FT NON_TER 1 115
SQ SEQUENCE 115 AA; 13616 MW; F8E7A05958C23D23 CRC64;

Query Match	10.9%	Score 171	DB 3	length 115
Best Local Similarity	34.3%	Pred. No. 1.1e-07		
Matches 37	Conservative 19	Mismatches 48	Indels 4	Gaps 2

[illegible]

RESULT	15
09ZW22	
ID	09ZW22
AC	09ZW22; PRELIMINARY; PRT; 253 AA.
DT	01-MAY-1999 (TREMBLrel, 10, Created)
DT	01-MAY-1999 (TREMBLrel, 10, Last sequence update)
DT	01-JUN-2001 (TREMBLrel, 17, Last annotation update)
DE	PUTATIVE C-4 STEROL METHYL OXIDASE.
GN	Fl6p2.23.
OS	Arabidopsis thaliana (Mouse-ear cress).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC	rosids II; Brassicales; Brassicaceae; Arabidopsids.
OX	NCBI_TaxId=3702;
XX	[1]
XX	SEQUENCE FROM N.A.
RP	STRAIN=CV. COLUMBIA.
RA	Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
RA	Shen M., Ronning C.M., Fraser C.M., Somerville C.R., Venter J.C.;
RT	"Arabidopsis Thaliana chromosome II BAC Fl6p2 genomic sequence.";
RL	Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RL	EMBL: AC004561; AAC95199.1; -
DR	InterPro: IPR001541; Sterol desat.
DR	Pfam: PF01598; Sterol desat; 1.
Q0	SEQUENCE 253 AA; 25477 MW; E2B389CD06D59645 CRC64;

Query Match	10.7%	Score 167;	DB 10;	Length 253;
Best Local Similarity	22.2%;	Pred No 5.7e-07;		
Matches 58;	Conservative 32;	Mismatches 75;	Indels 96;	Gaps 11;

QY	52	LYFSGGLMGF-----	YUYLKINVLPRDAIPTIK	82
Db	26	VFFLSGRLYFLFERTGSLNKTQTKSNTPEAOGSKTARLLLYNHCYNLRLMAASTYVFR	YUYLKINVLPRDAIPTIK	85
QY	83	AMRLQMFVAMKARWYTLPTVSESMIERGWTCFASIDFGWTLVFVYIATLVLEVEFG	YUYLKINVLPRDAIPTIK	142
Db	86	FMGME-----SSFP-----LPS-----	YUYLKINVLPRDAIPTIK	115
QY	143	IYMHRELHDKRLPYKYLNTNHNLYNKONTLSRA-----	YUYLKINVLPRDAIPTIK	190
Db	116	FYMGHRLILH-TKMLYIKVAVSHNHEY-----	YUYLKINVLPRDAIPTIK	168
QY	191	VPHVIALFIVPIHFTTHIGLLEMEATWTANIHDICIH-----	YUYLKINVLPRDAIPTIK	243
Db	170	GRHLITLML-----	YUYLKINVLPRDAIPTIK	219
QY	244	--FYKNHNGYNTIMDMFGS	YUYLKINVLPRDAIPTIK	262
Db	220	LYTSGNISSTFYMDMIFGT	YUYLKINVLPRDAIPTIK	240

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 4, 2002, 17:06:27 ; Search time 9.86 Seconds

(without alignments)
1044.910 Million cell updates/sec

Title: US-09-775-879-21

Perfect score: 1562

Sequence: 1 MADNAYLMQFVDETSFYNR.....SLRDLLEEDNDKDSFKAE 281

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 3664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	341	21.8	299	1 SC5D_MOUSE	O88822 mus musculu
2	330	21.1	299	1 SC5D_HUMAN	O75845 homo sapien
3	309.5	19.8	364	1 ERG3_CANGA	P50860 candida gla
4	304.5	19.5	329	1 ERG3_SCHPO	O13666 schizosacch
5	295.5	18.9	365	1 ERG3_YEAST	P32353 saccharomyc
6	156	10.0	293	1 ER25_HUMAN	O15800 homo sapien
7	152.5	9.8	309	1 ER25_YEAST	P53045 saccharomyc
8	141.5	9.1	308	1 ER25_CANAL	O59933 candida alb
9	117	7.5	349	1 SUR2_YEAST	P38992 saccharomyc
10	98	6.3	615	1 YKH0_YEAST	P25956 saccharomyc
11	98	6.3	615	1 YKH6_YEAST	P32173 saccharomyc
12	92.5	5.9	542	1 LMT_YEAST	O90188 chlamydia m
13	91	5.8	534	1 TNH1_YEAST	P53322 saccharomyc
14	90.5	5.8	279	1 YRR6_MYCA	P43045 mycoplasma
15	90	5.7	265	1 COX3_MARPO	P26858 marichantia
16	89	5.7	649	1 COX1_BACSU	P34956 bacillus su
17	88.5	5.7	308	1 COX3_PONPA	O21403 struthio ca
18	87.5	5.6	261	1 COX3_STRCA	P92896 pongo pygma
19	87	5.6	261	1 COX3_PONPA	P33303 anopheles q
20	87	5.6	341	1 CYB_GYMTI	P29637 gymnotina
21	86	5.5	308	1 CYB_ANOQU	O76024 homo sapien
22	86	5.5	369	1 WFS1_HUMAN	O08675 mus musculu
23	85	5.4	369	1 PAR3_MOUSE	O84539 chlamydia t
24	85	5.4	542	1 LMT_YEAST	O37620 protoliteca
25	84.5	5.4	805	1 DF19_CAEEL	O09555 caenorhabdi
26	84.5	5.4	805	1 COX3_RHIST	P80441 rhizopus st
27	84	5.4	281	1 COX3_ARATH	P92514 arabidopsis
28	83.5	5.3	265	1 CYB_CHRVI	O03215 chromatiu
29	83.5	5.3	411	1 PDRC_YEAST	O02785 saccharomyc
30	83.5	5.3	255	1 RCBM_RHOPH	P51751 rhodospirill
31	83	5.3	465	1 GAR2_HUMAN	P28476 homo sapien
32	83	5.3	465	1 ARE1_YEAST	P25628 saccharomyc
33	83	5.3	610	1 ARE1_YEAST	P25628 saccharomyc

34	82.5	5.3	353	1 CKR8_MOUSE	P56484 mus musculu
35	82.5	5.3	580	1 P69_MYCHR	P15362 mycoplasma
36	82	5.2	338	1 YVAD_BACSU	P37520 bacillus su
37	81.5	5.2	329	1 COX3_ACACA	O37374 acanthamoeb
38	81.5	5.2	581	1 FUR4_SCHPO	O10279 schizosacch
39	81.5	5.2	2273	1 HPA1_YEAST	P32874 saccharomyc
40	81	5.2	269	1 COX3_EMENT	P00421 emeticella
41	81	5.2	560	1 YG14_YEAST	P53154 saccharomyc
42	81	5.2	824	1 SIIP_SALTY	O92HC7 salmonella
43	80.5	5.2	374	1 PAR3_HUMAN	O00254 homo sapien
44	80.5	5.2	392	1 CYB_SOLTU	P29757 solanum tub
45	80.5	5.2	465	1 GAR2_MOUSE	P56476 mus musculu

ALIGNMENTS

RESULT 1	ID	SC5D_MOUSE	STANDARD;	PRT;	299 AA.
AC	O88822:	SC5D_MOUSE			
DT	15-JUL-1999	(Rel. 38, Created)			
DT	15-JUL-1999	(Rel. 38, Last sequence update)			
DT	20-AUG-2001	(Rel. 40, Last annotation update)			
DE	LATHOSTEROL OXIDASE (EC 1.3.3.2) (LATHOSTEROL 5-DESATURASE) (STEROL 5-DESATURASE)				
GN	SC5DL OR SC5D				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;				
OX	NCBI_Taxid=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=BALB/C;				
RA	Nishit S., Nishino H., Ishibashi T.;				
RT	"Molecular cloning and expression of the human and mouse lathosterol				
RT	5-desaturase.";				
RL	Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.				
CC	- 1- CATALYTIC ACTIVITY: 5-ALPHA-CHOLEST-7-EN-3-BETA-OL + O(2) =				
CC	CHOLESTA-5,7-DIEN-3-BETA-OL + H(2)O(2).				
CC	- 1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. ENDOPLASMIC				
CC	RETICULUM (PROBABLE).				
CC	- 1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE				
CC	AND/OR BE INVOLVED IN METAL ION BINDING.				
CC	- 1- SIMILARITY: BELONGS TO THE STEROL DESATURASE FAMILY.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL: AB016248; BAA33730.1; -				
DR	MGD: MGI:1353611; SC5d.				
DR	InterPro: IPR001541; Sterol_desat.				
DR	Plan: P01598; Sterol_desat; 1.				
KW	Sterol biosynthesis; Oxidoreductase; Endoplasmic reticulum; Iron;				
KW	Transmembrane.				
FT	TRANSMEM 32 52				POTENTIAL.
FT	TRANSMEM 79 99				POTENTIAL.
FT	TRANSMEM 117 137				POTENTIAL.
FT	TRANSMEM 186 206				POTENTIAL.
FT	DOMAIN 138 143				HISTIDINE BOX 1.
FT	DOMAIN 151 155				HISTIDINE BOX 2.
FT	DOMAIN 228 233				HISTIDINE BOX 3.
SO	SEQUENCE 299 AA; 35062 MW; C6B3BBAA44D58E177 CRC64;				

Query Match 21.8%; Score 341; DB 1; Length 299;
Best local Similarity 33.2%; Pred. No. 1.4e-19;

[illegible]

```

RESULT 2
SC5D_HUMAN STANDARD: PRT; 299 AA.
AC 075845; 000119;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE LATHOSTEROL OXIDASE (EC 1.3.3.2) (LATHOSTEROL 5-DESATURASE) (DELTA-7-
DE STEROL 5-DESATURASE) (C-5 STEROL DESATURASE) (STEROL-C5-DESATURASE).
CN SC5DL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Nishi S., Nishino H., Ishibashi T.;
RT "Molecular cloning and expression of the human and mouse lathosterol
RT 5-desaturase.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-97130614; PubMed-8976377;
RA Matsushima M., Inazawa J., Takahashi E., Suzumori K., Nakamura Y.;
RT "Molecular cloning and mapping of a human cDNA(SC5D) encoding a
RT protein homologous to fungal sterol-C5-desaturase.";
RL Cyogenet. Cell Genet. 74:252-254(1996).
CC -1- CATALYTIC ACTIVITY: 5-ALPHA-CHOLEST-7-EN-3-BETA-OL + O(2) =
CC -1- CHOLESTA-5,7-DIEN-3-BETA-OL + H(2)O(2).
CC -1- COFACTOR: IRON (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. ENDOPLASMIC
CC RETICULUM (PROBABLE).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: BELONGS TO THE STEROL DESATURASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AB016247; BAA33729.1; -
DR EMBL: D85181; BAA18970.1; -.
DR MIM: 602286; -.
DR InterPro: IPR001541; Sterol_desat.
DR Pfam: PFO1598; sterol_desat; 1.

```

KM	Steryl biosynthesis; Oxidoreductase; Endoplasmic reticulum; Iron;
KW	transmembrane.
FT	TRANSMEM 32 52 POTENTIAL.
FT	TRANSEM 79 99 POTENTIAL.
FT	TRANSEM 117 137 POTENTIAL.
FT	TRANSEM 186 206 POTENTIAL.
FT	DOMAIN 138 143 HISTIDINE BOX 1.
FT	DOMAIN 151 155 HISTIDINE BOX 2.
FT	DOMAIN 228 233 HISTIDINE BOX 3.
FT	CONFLICT 216 299 POLIPEPTIDESAHHTDHHMFQYNYGOVFTLMDRIIGSSPKK PSSEFGKGRPLYAKMETBEKRSSPSSGCKNKKLNGEFTT TE -> RKKYSMESLDQRNLRLIPST (IN REF. 2).
SQ	SEQUENCE 299 AA; 35261 MW; 9EFB21EE3EFAF56 CR664;

Query Match	21.1%	Score	330	DB	1	Length	299
Best Local Similarity	32.9%	Pred. NO.	1e-16	73			
Matches	82	Conservative	52	Mismatches	73	Indels	42
						Gaps	12

```
QY      51 LWFELSGFMCFIY-----YLKINVLYLPKAIFTIKANRLQWAMKAMPWTLL 101  
       :| | | :| | | :| | |  
Db     44 ILFFCATLSYFVFDHALMKHDFLKNQV-----RRRIETFTVALPWSITL 90
```

```
QY      102 PTVESMIE-RGWTKCFASIDEFGMLFYVYIAI-YLVEVEFGIYMMHRELHDIKPLYK 156
        || : ::|||::| : || : | : : : | : | : |||::|| : : ||
Db       91 -TVAALFLEINIGYSKLHLDGEPYPGLFEELVWSIISFLFTDMFIWIHRGH-H-RLVYK 148
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```

QY 159 YLHATHNIYNKQNTLSPEFAGLAFNRVDGILQAVRNVIALEIVRIHFTTHIGLLFMEAIWT 218
    || ||| :||| ||||:| |:::| | | | : : : |||
Db 149 RLHKRHHNI--KIPRFASHAFNRIDGLOSRLPHIYRIFRPLKRVVLSLYILVNIWT 205

```

OY 219 ANIHDCI HGN----- IWP-VMGAGYHTT HTTYKHN GCH- T INMDMFESLRDPLLEE 270
 :||| | : | : ||| | | : ||| | | : ||| |
Dd 206 ISIH--GDRVPOLIOPIFNGSAHHDHDMFEFDYNQGYETIA-W-DRIGSSEKNPSSFF 261

QY	271	DDNKDSFK	279
		:	
Db	262	GKGPISYVK	270

RESULT 3

ID	ERG3_CANGA	STANDARD;	PRT;	364 AA.
AC	P50860;			
DT	01-OCT-1996	(Rel. 34, Created)		

DT 20-AUG-2001 (Rel. 40, last annotation update)
DE C-5 STEROL DESATURASE (EC 1.3.-.-) (STEROL-C5-DESATURASE).
GN ERG3.

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5478;

RP SEQUENCE FROM N.A.
RC STRAIN=2001-L5;
RX MEDLINE=96161286; PubMed=8593007;

RT viability cell growth, sterol composition, and antifungal

CC -I- FUNCTION: CATALYZES THE INTRODUCTION OF A C-S DOUBLE BOND IN THE
RING OF EPICHAETIDIOL MAY CONTRIBUTE TO THE REGULATION OF
CC Antimicrob. Agents Chemother. 39:2708-2717(1995).

```

CC      ERGOSTEROL BIOSYNTHESIS.
CC      -|- COFACTOR: IRON (BY SIMILARITY).
CC      -|- PATHWAY: ERGOSTEROL BIOSYNTHESIS.
CC      -|- SUBSTRATE: ERGOSTEROL BIOSYNTHESIS.

```

CC RETICULUM (PROBABLE).
CC -I- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC

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CC -----
DR EMBL; L40390; AAB02330.1; -
DR InterPro; IPR001541; Sterol_desat.
DR Pfam; PF01598; Sterol_desat; 1.
KM Sterol biosynthesis; Oxidoreductase; Endoplasmic reticulum; Iron;
KM Transmembrane.
FT TRANSMEM 94 114 POTENTIAL.
FT TRANSMEM 142 162 POTENTIAL.
FT TRANSMEM 249 269 POTENTIAL.
FT DOMAIN 201 205 HISTIDINE BOX 1.
FT DOMAIN 214 218 HISTIDINE BOX 2.
FT DOMAIN 289 293 HISTIDINE BOX 3.
SQ SEQUENCE 364 AA; 42735 MW; 91010FD86BC137F0 CRC64;

Query Match 19.8%; Score 309.5; DB 1; Length 364;
Best Local Similarity 31.2%; Pred. No. 4.6e-17;
Matches 89; Conservative 46; Mismatches 103; Indels 47; Gaps 11;

OY 7 YLMQVDETSFYNRIVLSHLPLANLMEPLPHLOTWLRNYLAGTLTYFISGLMCTYIY- 65
DB 72 FLEDETEKT-----YASLLEPRN--NLIRREFSLAAVTVFGLLITLTAASYVEVD 122
OY 66 -----YLKINVYLPKRAIPTIKAMRLQMFYAMKAMPWYLLLPVSSSMIE-RGWTGC 116
DB 123 RIFNHPKILKMQM-----LEIKLAWSAIPFMSTL-TVPMFLMLNCTISKL 168
OY 117 FASID--EFGWILYFYVYAIYLVFEVEGTYMMHRELHDIKPLYKYLAATHHYNKONTLS 174
DB 169 YVDVDMENHGRLKRLIEVATFTFTCGIYLAHRMLHWPR--YKALHKRPH--KMLVYC 224
OY 175 PRAGLAFHNVDSILOAVPVALFVPIHFTTHIGLLEMAIVTANIHDCIGNINPVM- 233
DB 225 PRASHAFHNVDSYFQSLASHIYPMILPLKHSIYLILFTVENFWSVMIHGQHSNNPVNA 284
OY 234 GAGYFTHHTHTTKYKNYGHYTIWDMWFGSLR-----DPLLEED 271
DB 285 GTACHTVHHLFYNNYNGOFTTLMDRIGSYRPPEDSLPDKLMD 329

RESULT 4
ERG3_SCHPO STANDARD; PRT; 329 AA.
AC 013666;
DT 15-JUL-1999 (Rel. 38; Created)
DT 15-JUL-1999 (Rel. 38; Last sequence update)
DT 20-AUG-2001 (Rel. 40; Last annotation update)
DE PROBABLE C-5 STEROL DESATURASE (EC 1.3.-.-) (STEROL-C5-DESATURASE).
GN SPCB27812.03C OR PI075.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Kushiida N., Yamazaki S., Tanaka T., Jinno K., Haikawa Y., Yamazaki J.,
RA Yamamoto S., Sekine M., Oguchi A., Nagai Y., Sakai M., Aoki K.,
RA Ogura K., Otsuka R., Kudoh Y., Yanagida M., Machida M., Zhang M.Q.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Wood V., Rajadream M.A., Barrell B.G., Lauber J., Hilbert H.,

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RA Duesterhoeft A.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC - FUNCTION: CATALYZES THE INTRODUCTION OF A C-5 DOUBLE BOND IN THE B
CC RING OF ERGOSTEROL. MAY CONTRIBUTE TO THE REGULATION OF
CC ERGOSTEROL BIOSYNTHESIS (BY SIMILARITY).
CC - COFACTOR: IRON (BY SIMILARITY).
CC - PATHWAY: ERGOSTEROL BIOSYNTHESIS.
CC - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. ENDOPLASMIC
CC RETICULUM (PROBABLE).
CC - DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC - SIMILARITY: BELONGS TO THE STEROL DESATURASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB004539; BAA21457.1; -
DR EMBL; AL021766; CAA16898.1; -
DR InterPro; IPR001541; Sterol_desat.
DR Pfam; PF01598; Sterol_desat; 1.
KM Sterol biosynthesis; Oxidoreductase; Endoplasmic reticulum; Iron;
KM Transmembrane.
FT TRANSMEM 67 87 POTENTIAL.
FT TRANSMEM 149 169 POTENTIAL.
FT TRANSMEM 210 230 POTENTIAL.
FT DOMAIN 170 175 HISTIDINE BOX 1.
FT DOMAIN 183 187 HISTIDINE BOX 2.
FT DOMAIN 257 262 HISTIDINE BOX 3.
SQ SEQUENCE 329 AA; 39063 MW; C9DEF93732BC4BFA CRC64;

Query Match 19.5%; Score 304.5; DB 1; Length 329;
Best Local Similarity 31.2%; Pred. No. 1e-16;
Matches 85; Conservative 53; Mismatches 107; Indels 27; Gaps 12;

OY 3 ADNAYLMQVDETSFYNRIVLSHLPLA-NLMEPLPH-FLOTWLRNYLAGTLTYFISGLW 60
DB 34 AVNSTGLGLAEKYNF--AITSGLLDRNNVWRQTSFLITW---LWGLSYFLSA-SF 85
OY 61 CFYIYIKINIVLPKRAIPTIKAMR-----LQMFYAMKAMPWYLLLPVSSSMIE-RGWTGC 115
DB 86 AYYVYEDR-----EEARRHPKFLKQNHLELWALNKLPGMAL--TAPFELAEIRGQY 138
OY 116 CFASIDFEGWILYFYVYAIYLVFEVEGTYMMHRELHDIKPLYKYLAATHHYNKONTLS 175
DB 139 VYKLDYEGYFYLPFSIALFLFSDFLITWIRALNH-RWLYAPLNLH--KWIVPTP 194
OY 176 FAGLAFHNVDSILOAVPVALFVPIHFTTHIGLLEMAIVTANIHDCIH-GNINPVMG 234
DB 195 YSSHAFFYLDGYSQSLPYHMFPEFFPKNKVYLLPFSQVYMWYLLIRDGAFYSNNAVNG 254
OY 235 AGYHTHTHTTKYKNYGHYTIWDMWFGSLRP 266
DB 255 AAHHAHHMWFNNYNGOFTLFPRLCSSYROP 286

RESULT 5
ERG3_YEAST STANDARD; PRT; 365 AA.
AC P32353;
DT 01-OCT-1993 (Rel. 27; Created)
DT 01-OCT-1993 (Rel. 27; Last sequence update)
DT 20-AUG-2001 (Rel. 40; Last annotation update)
DE C-5 STEROL DESATURASE (EC 1.3.-.-) (STEROL-C5-DESATURASE).
GN ERG3 OR STR1 OR YLR056W OR L2150.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetaceae.

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OX NCBI_TaxID=49932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91323727; PubMed=1864507;
RA Arthington B.A., Bennett L.G., Skatrud P.L., Guynn C.J., Barduch R.J.,
RA Ulbright C.E., Baird M.;
RT "Cloning, disruption and sequence of the gene encoding yeast C-5
RT sterol desaturase.";
RL Gene 102:39-44(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA Renauld G., Lacroste F., Cassart J.P., Vandenhaute J., Delcour J.;
RL Submitted (MAR-1992) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=94236239; PubMed=8180700;
RA Taguchi N., Takano Y., Julmanop C., Wang Y., Stock S.,
RA Takemoto J.Y., Miyakawa T.;
RT "Identification and analysis of the Saccharomyces cerevisiae SYR1
RT gene reveals that ergosterol is involved in the action of
RT syringomycin.";
RL Microbiology 140:353-359(1994).
RN [4]
RP SEQUENCE FROM N.A.
RA Andre B., Urestarazu L.A.;
RL Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: CATALYZES THE INTRODUCTION OF A C-5 DOUBLE BOND IN THE B
CC RING OF ERGOSTEROL. MAY CONTRIBUTE TO THE REGULATION OF
CC ERGOSTEROL BIOSYNTHESIS.
CC -1- COFACTOR: IRON (BY SIMILARITY).
CC -1- PATHWAY: ERGOSTEROL BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. ENDOPLASMIC
CC RETICULUM (PROBABLE).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: BELONGS TO THE STEROL DESATURASE FAMILY.
CC -----
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CC -----
DR EMBL; M62623; AAA34894.1; -
DR EMBL; S46162; AAB39844.1; -
DR EMBL; M64989; AAA34595.1; -
DR EMBL; D14299; BAA2092.1; -
DR EMBL; X94607; CAA64303.1; -
DR EMBL; Z73328; CAA97586.1; -
DR PIR; J01146; J01146.
DR PIR; S41993; S41993.
DR SGD; S0004046; ERG3.
DR InterPro; IPR001541; Sterol_desat.
DR Pfam; PF01598; Sterol_desat; 1.
KW Sterol biosynthesis; Oxidoreductase; Endoplasmic reticulum; Iron;
KW Transmembrane
FT TRANSMEM 93 113
FT TRANSMEM 141 161 POTENTIAL.
FT TRANSMEM 243 263 POTENTIAL.
FT DOMAIN 200 204 HISTIDINE BOX 1.
FT DOMAIN 213 217 HISTIDINE BOX 2.
FT DOMAIN 288 292 HISTIDINE BOX 3.
SQ SEQUENCE 365 AA; 42730 MW; 76441DA6927A711C CRC64;

Query Match	18.9%	Score 295.5;	DB 1;	Length 365;
Best Local Similarity	31.5%;	Pred. No. 5.5e-16;		
Matches 87;	Conservative 43;	Mismatches 95;	Indels 51;	Gaps 12;
QY	15	TSPFNRIYSLHPALNWEPPHPIQIOTWLRNVLACTLLTYISGIFMCFYIY-----	65	

ID	ER25_HUMAN	STANDARD:	PRT:	293 AA.
Db	78	TSF-----ASLLPRS--SILREFISLWIVITFGLLLVLFASLSYVFVFOKSIINHR	129	
Oy	66	YKINVLPEKDAIPITKAMRLQMFVAMKAMPYTLLEPYSEKIE-RGKTCFASIDERG	124	
Db	130	YLR-----NOMAEIKLAVSAIPWMSML-TVPWFVEMELGSHSKLYMKIDYEN	175	
Oy	125	W-----ILYEVYIAIYLVFVEEGIYWMRELHDIDIKPKLYLHATHTINKOMTLSPPG	178	
Db	176	HQVRLILIEYFFI-----FFTDQGYLAHRLHWR-VYRALHKPHN---KWLVCFFPS	227	
Oy	179	LAHPHVDGILQAVPHVIALEFIVPIHETTHIGLLEMAIWTANIHCIDH-GNIWPVAGY	237	
Db	228	HSFHFVDGLOLSIYHIVLPLPLHKVSYLLETFEVPFWTMVIMHDQYLSNPNVAGTAC	287	
Oy	238	HIHHTTKHNYGHTIMWDMFGSLRDLLEEDN	273	
Db	288	HTVHLLYENYNGOFTTMDRLGGSYRRP---DDS	319	
RESULT	6			
ER25_HUMAN		STANDARD:	PRT:	293 AA.
AC	Q15800:			
DT	01-NOV-1997	(Rel. 35, Created)		
DT	01-NOV-1997	(Rel. 35, Last sequence update)		
DT	20-AUG-2001	(Rel. 40, Last annotation update)		
DE	C-4 METHYL STEROL OXIDASE (EC 1.1.1.171).			
GN	SCAMOL OR ERG25 OR DESP4.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Intestine;			
RX	MEDLINE=96279274; PubMed=8663358;			
RA	Li L., Kaplan J.;			
RT	"Characterization of yeast methyl sterol oxidase (ERG25) and			
RT	identification of a human homologue.";			
RL	J. Biol. Chem. 271:16927-16933(1996).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Retina;			
RA	Herrmann K.;			
RL	Submitted (MAR-1997) to the EMBL/Genbank/DBJ databases.			
CC	-1- COFACTOR: IRON (PROBABLE).			
CC	-1- PATHWAY: CHOLESTEROL BIOSYNTHESIS.			
CC	-1- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED; ENDOPLASMIC RETICULUM.			
CC	-----			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: U60205; AAC50587.1; -;			
DR	EMBL: U93162; AAB81566.1; -;			
DR	InterPro: IPR001541; Sterol_desat.			
DR	Plam; PF01596; Sterol_desat; 1.			
KW	Sterol biosynthesis; Oxidoreductase; Transmembrane; Iron.			
FT	CARBOYD 4 4			
FT	CARBOYD 4 3			
FT	TRANSMEM 55 75			
FT	TRANSMEM 199 219			
FT	SEQUENCE 293 AA; 35215 MW; D88EDDD8E5DE0BF CRC64;			

Query Match	10.0%;	Score 156;	DB 1;	Length 293;
Best Local Similarity	22.8%;	Pred. No. 2.4e-05;		
Matches 74;	Conservative 41;	Mismatches 110;	Indels 100;	Gaps 16;

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QY 9 MOFVDETSFYNRIVLSHLLPAN-LMEPLRPHLOTWLRNYLA-----GTL-----LYF-- 54
DB 17 VEYVDS-----LLPENRLOEPFKNANNYMLNNTTKROLATWGSLLIHEALYLF 65
QY 55 -ISGFLKCFYIYKINYLPRDAIPT-----IKARLOMF----- 89
DB 66 CLPGLFQFIPRPMKKYKI--QKDKREPTWEMQKCKVLLFNHFCIOLPLICGTYPTFEYF 123
QY 90 ---VAMKAMP--WYLLPVSSESMIERGWTGCF--ASIDEQGLLYFYIAYLVFVFGIY 144
DB 124 NIPYMERKPRMYELL-----ARCGCAVIEDTW-----HY 154
QY 145 WMHRELHDIKPLKYKLAHTHHYKNTLSPFAGLA--FHPYDGILOAVPHYALFIVPI 202
DB 155 FLHRLHMH-KRKYKYLHNHVEFQ-----APFGMEAEVHNPLETLLIGGFFIGIYLLCD 208
QY 203 HFTTHIGLFEALFTANIHDCIHGNIMPV-----MGAGYPTIHHTYKHNHYGHTYIM 256
DB 209 HVILLMAVVTIRLLETIVHSGYDIPLNPLNLIPYAGSRHHDHFMHFNIGVASTFTWM 268
QY 257 DMMEGSLDPLLEDDNKDSFKKAE 281
DB 269 DRIFGTSQYNAVYNEKKRKKFEKTE 293

RESULT 7
ER25_YEAST STANDARD: PRT: 309 AA.
AC P53045;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE C-4 METHYL STEROL OXIDASE (EC 1.-.-.-).
GN ERG25 OR FET6 OR YGR060W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
[1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96133902; Pubmed=8552601;
RA Bard M., Bruner D.A., Pierson C.A., Lees N.D., Biermann B., Frye L.,
RA Koegel C., Barbuch R.;
RT "Cloning and characterization of ERG25, the Saccharomyces cerevisiae
RT gene encoding C-4 sterol methyl oxidase.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:186-190(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Entlan K.D., Rose M., Koetter P., Roehmer A., Sehram I., Hempel S.;
RL Submitted (May-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RA LI L., Kaplan J.;
RA MEDLINE=96279274; Pubmed=8663358;
RT "Characterization of yeast methyl sterol oxidase (ERG25) and
RT identification of a human homologue";
RL J. Biol. Chem. 271:16927-16933(1996).
CC -1- FUNCTION: CATALYZES THE FIRST STEP IN THE REMOVAL OF THE TWO C-4
CC METHYL GROUPS OF 4,4-DIMETHYLYZMOSTEROL.
CC -1- COFACTOR: IRON.
CC -1- PATHWAY: ERGOSTEROL BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM (PROBABLE).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: BELONGS TO THE STEROL DESATURASE FAMILY.
CC -----
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CC -----
DR EMBL: U31885; AAC49139.1;
DR EMBL: 272845; CAA97062.1;
DR SGD: S0003292; ERG25.
DR InterPro: IPR001541; Sterol_desat.
DR Pfam: PF01598; Sterol_desat; 1.
KW Sterol biosynthesis; Oxidoreductase; Endoplasmic reticulum;
KW Transmembrane; Iron.
FT TRANSMEM 56 76 POTENTIAL.
FT DOMAIN 160 164 HISTIDINE BOX 1.
FT DOMAIN 173 177 HISTIDINE BOX 2.
FT DOMAIN 257 263 HISTIDINE BOX 3.
SQ SEQUENCE 309 AA; 36479 MW; E0422CA16DD17794 CRC64;

Query Match 9.8%; Score 152.5; DB 1; Length 309;
Best Local Similarity 20.4%; Pred. No. 4,6e-05;
Matches 68; Conservative 55; Mismatches 111; Indels 99; Gaps 16;

QY 15 TSFYNRIVLSHLLPANL-----WEPLRPHLO-----TWLRNYLAGTLVFISS 57
DB 2 SAVFNNAITSLGLVQASTYSQTLONVAHYOPOLNFMEXYMAWYSYMNNDVLAGLMF--- 58
QY 58 FLWCFYIYKINYLPRDAIPTIKARLOMFVAMKAMPYLLPVSSESMIERGWTGCF 117
DB 59 FLHHEMFYFRCPLPWFIIIDIPYFRKKLOP-----TKIPSAKBDLY-----CL 102
QY 118 AST-----DEFGMILFYVYIAYLVFVERGI-----YMHRE 149
DB 103 KSVLLSHFLVEAIPITWTFHPRMCEKLGITVEVPPPSLKTMALEIGLFVLBDTWYMAHRL 162
QY 150 LHDIKRLKYKLAHTHHYKNTLSPFAGLA--FHPYDGI-----LOAVPHYALFIVP 201
DB 163 FH-YGVFYKYLHKQHRV-----AAPG-GSAAYAHAEFLSLGFTVSGPILYVMTGK 215
QY 202 IHFTT---HIGLFEAL-----WTANIHDCIHGNIMPV--MGAGYPTIHHTYKHN 248
DB 216 LHFILCVMTTLRLPQAVDSHSGYDFPWSLN-----KIMPMWAGAHHDHNNHYFIGN 268
QY 249 YGHYTTWMDMEGSLDPLLEDDNKDSFKKAE 281
DB 269 YASSFRWMDYCLDTESGPEAKASREBRMKRAE 301

RESULT 8
ER25_CANAL STANDARD: PRT: 308 AA.
AC 059933;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE C-4 METHYL STEROL OXIDASE (EC 1.-.-.-).
GN ERG25.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
[1]
RP SEQUENCE FROM N.A.
RA STRAIN=CAI-8;
RA Johnson T., Kennedy M.A., Lees N.D., Bard M.;
RT "ERG25, C-4 sterol methyl oxidase from Candida albicans.";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CATALYZES THE FIRST STEP IN THE REMOVAL OF THE TWO C-4
CC METHYL GROUPS OF 4,4-DIMETHYLYZMOSTEROL (BY SIMILARITY).
CC -1- COFACTOR: IRON (BY SIMILARITY).
CC -1- PATHWAY: ERGOSTEROL BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM (PROBABLE).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: BELONGS TO THE STEROL DESATURASE FAMILY.
CC -----
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CC -----
DR EMBL: AF051914; AAC06014.1; -
DR InterPro: IPR001541; Sterol_desat.
DR Pfam: PF01598; Sterol_desat; 1.
KW Sterol biosynthesis; Oxidoreductase; Endoplasmic reticulum;
KW Transmembrane; Iron.
FT TRANSMEM 56 76 POTENTIAL.
FT DOMAIN 160 164 HISTIDINE BOX 1.
FT DOMAIN 173 177 HISTIDINE BOX 2.
FT DOMAIN 257 263 HISTIDINE BOX 3.
SQ SEQUENCE 308 AA; 36561 MW; 45D7D7AE4081BC15 CRC64;

Query Match 9.18; Score 141.5; DB 1; Length 308;
Best Local Similarity 22.3%; Pred. No. 0.00032;
Matches 65; Conservative 38; Mismatches 95; Indels 93; Gaps 18;

QY 59 LMCFEYIYLKINYLPRDAIPTIKAMRLQMEVAMKAMPWTL-----LPT 103
DB 39 LKMSYIYTMANDLF-----ATGLFELTHEIEFGRCILPMALIDRIPYFRKKIKODEKIPS 94
QY 104 VSESMIERGWTGCFAS-----IDERG-WLY-----FVYIAIY 135
DB 95 DKBO-----W-ECLKSVLTHSHFLVEAPRPFHPLCKIGISYGVPPPKITDMLIQNAVF 148
QY 136 LVVEFGIYMKHRELNDIKLYKYLATHTIYNKONTLSPAGAA--FHVYDGL----- 188
DB 149 FVLEDTHWYHFNRLH-YGVFYKXIKHKNHRY-----AAPF-GIAAEYAHNEVALLGLG 201
QY 189 -QAVPHYALFIVPIHTHTHIGLFEAMV-----TANHD-----CIHGINMPV-M 233
DB 202 TVGIPYIWCILTNLH-----LFTVSIWIIILFLQAVDHNHSGYEPFWSIH-NFLPWA 253
QY 234 GAGYHTIHTHTYKHNHYHTIWMDFGSLRDLLE---EDDNKDSFKAE 281
DB 254 GADHNDHNHYETIGYSSFRWMDFLDTEAGPRAKKRGREKXVAKQNEKLG 304

RESULT 9
SUR2_YEAST STANDARD; PRT; 349 AA.
ID SUR2_YEAST
AC P38992;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DE SUR2 PROTEIN (SYRINGOMYCIN RESPONSE PROTEIN 2).
GN SUR2 OR SYR2 OR YDR297W OR D9740.8.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RA SEQUENCE FROM N.A.
RC STRAIN=K21;
RA Desfarges L., Durens P., Juguelin H., Cassagne C., Bonneau M.,
RL Aigle M.;
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=K21-1C;
RX MEDLINE=97020262; PubMed=8868422;
RA Clifton P., Wang Y., Mochizuki D., Miyakawa T., Wangspa R.,
RT "Syr2, a gene necessary for syringomycin growth inhibition of
RT Saccharomyces cerevisiae."
RL Microbiology 142:477-484(1996).
RN [3]

RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA Favetto A., Fulton L., Gattung S., Greco T., Kirsten J.,
RA Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,
RA Johnson D., Johnston L., Langston Y., Latreille P., Le T.,
RA Madis E., Meneses S., Miller N., Nhan M., Pauley A., Peluso D.,
RA Riken L., Riles L., Taich A., Trevaskis E., Vignati D.,
RA Wilcox L., Wohldman P., Vaudin M., Wilson R., Waterston R.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INVOLVED IN THE RESPONSE TO SYRINGOMYCIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
CC -----
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CC -----
DR EMBL: U07171; AAA16608.1; -
DR EMBL: U10427; AAB41115.1; -
DR EMBL: U28374; AAB64733.1; -
DR PIR: S48533; S48533.
DR SGD: S0002705; SUR2.
DR InterPro: IPR001541; Sterol_desat.
DR Pfam: PF01598; Sterol_desat; 1.
KW Transmembrane.
FT TRANSMEM 9 29 POTENTIAL.
FT TRANSMEM 50 70 POTENTIAL.
FT TRANSMEM 99 119 POTENTIAL.
FT TRANSMEM 148 168 POTENTIAL.
FT TRANSMEM 209 229 POTENTIAL.
SQ SEQUENCE 349 AA; 40734 MW; 406D778092CA75C1 CRC64;

Query Match 7.58; Score 117; DB 1; Length 349;
Best Local Similarity 21.9%; Pred. No. 0.028;
Matches 66; Conservative 55; Mismatches 114; Indels 66; Gaps 17;

QY 3 ADMNYLMGFVDETSP-----YNRIVLSHLPRANLMPRLPHLOTWLRNLTAGTLLYF-ISG 57
DB 9 AAGSPFLAFLGKLTSGEYHAKAPAINLRK---ESLRLPMSDGLVALVAPVAVWALSG 65
QY 58 LMCFEYIYL--KINVLPRDAIPTIKAMRLQMEVAMKAMPWTLPTVSESMT----- 109
DB 66 IFHYIDTHLAEKRIHSESEVAKRNKASRMHVFLEV-----ILQHIQIVGLIMH 118
QY 110 -----ERGWTKCFASIDE-----FGWILYVYTAIY--LVVEFGIYMHRE 149
DB 119 FEPYIMTGFEEENAMWKLRADLPRIIPDAIYGYWYGSAALKIFAGFLVDVWQYFLHRL 178
QY 150 LHDKPLKYYLHATHIYNKONTLSPFA-GLA-FHPVG-ILQAVPHYALFIVPIHTT 206
DB 179 MMNKTLLKMFHSVNH-----ELIYVYVYALFENPVGFLDITGISTAMTLHTHRE 233
QY 207 HIGLFEAMVITANTHDCIHGINMPV-----MGAGYHTIHTTY--KHNVGH--YTI 254
DB 234 QILTFEFAIMKTVDH-C--GYALPLDFQMLFPNNAVYHHIHQGFQIKNFAPFTFE 290
QY 255 W 255
DB 291 W 291

RESULT 10
YCHO_YEAST STANDARD; PRT; 615 AA.
ID YCHO_YEAST
AC P25596; P25597; P25599; P87002;
DT 01-MAY-1992 (Rel. 22, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)

```

DE HYPOTHEICAL 68.9 KDA PROTEIN IN HML 5' REGION.
NC YC1073C OR YC170C/YC171C/YC173C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA van der Aart O.T.M., Steensma H.V.;
RL Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP REVISIONS.
RA Gromada R.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE YC170C/YH1047C/YKR106W FAMILY.
CC -----
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CC -----
DR EMBL; X59720; CAA42397.1; -.
SD SGD; S0000575; YC1073C.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 59 79 POTENTIAL.
FT TRANSMEM 121 141 POTENTIAL.
FT TRANSMEM 153 173 POTENTIAL.
FT TRANSMEM 187 207 POTENTIAL.
FT TRANSMEM 217 237 POTENTIAL.
FT TRANSMEM 276 296 POTENTIAL.
FT TRANSMEM 308 328 POTENTIAL.
FT TRANSMEM 344 364 POTENTIAL.
FT TRANSMEM 384 404 POTENTIAL.
FT TRANSMEM 409 429 POTENTIAL.
FT TRANSMEM 441 461 POTENTIAL.
FT TRANSMEM 472 492 POTENTIAL.
FT TRANSMEM 548 568 POTENTIAL.
SQ SEQUENCE 615 AA; 68868 MW; D862B405FFDC9F12 CAC64;

Query Match 6.3%; Score 98; DB 1; Length 615;
Best Local Similarity 23.7%; Pred. No. 1.4;
Matches 62; Conservative 34; Mismatches 98; Indels 68; Gaps 13;

OY 24 SHLLPANI-----WEPLPHLQTLWRNYLAGTLTYISGLMCEFYIYLYKINVLPRDA 77
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 332 SPLPLFKLLSDRGIAWAP-----LGVTFENPFTFFISCOYLVPLL-VSMKESS 378
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY 78 IPTIKAMLLQMFVANKAPWITLPTVESMERGWTGCFASIDFGMLTFVYIAIYLV 137
   : : : : : | | | | | : : : : : : : : : : : : : : : : : : :
DB 379 TSAAMIVNLPGVAATASPFYSLVAKTRKLLSYIGCAA-----WM----- 421
   : : : : : | | | | | : : : : : : : : : : : : : : : : : : :

OY 138 FVEEFGYMHRELHDIKRYKYL--HATHHIIYKNKNTLSPFAG-LAFHPVDDIIGAV-PH 193
   ||| : : : | | | | | : : : : : : : : : : : : : : : : : :
DB 422 -VCNCLF-----YKRGSSGSHGVYIASVIMGLSGLLCSNSYIVITLQAMTH 468
   : : : : : | | | | | : : : : : : : : : : : : : : : : : :

OY 194 VIALFVPIHFT---THIGLFMEAIWTANIHDCIGHNIWPNVAGAGYHTIHTTYKHN 248
   ||| : : : | | | | | : : : : : : : : : : : : : : : : : :
DB 469 SRMAVITIGIQTFSKLGAIASVGAIAWTCMPNQLYKNL-----GNDTLAEIAYV-- 520
   || : : : | | | | | : : : : : : : : : : : : : : : : : :

OY 249 YGHYITMDMMFGS-LRDPLE 269
   || : : : | | | | | : : : : : : : : : : : : : : : : : :
DB 521 -SPYTFISDYFPGSPERDAVVE 541
   || : : : | | | | | : : : : : : : : : : : : : : : : : :

RESULT 11
YK86_YEAST STANDARD: PRT; 615 AA.
ID YK86_YEAST
DC P36173;

```

DT	01-JUN-1994 (Rel. 29, Created)
DT	01-JUN-1994 (Rel. 29, Last sequence update)
DT	01-FEB-1996 (Rel. 33, Last annotation update)
DE	HYPOTHETICAL 69.0 KDA PROTEIN IN SIR1 3' REGION.
GN	YKR106W.
OS	Saccharomyces cerevisiae (Baker's yeast).
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC	Saccharomycetales; Saccharomycetaceae; Saccharomycos.
OX	NCBI_TaxID=4932;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Gallion L., Dujon B.;
RL	Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC	-1- SIMILARITY: BELONGS TO THE YCL70C/YHR1047C/YKR106W FAMILY.
CC	-----
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CC	or send an email to license@sib-sib.ch).
CC	-----
DR	EMBL; Z28202; CAA82047.1; -.
DR	PIR; S40624; S40624.
DR	SCD; S0001814; YKR106W.
KW	Hypothetical protein; Transmembrane.
FT	TRANSMEM 59 79 POTENTIAL.
FT	TRANSMEM 121 141 POTENTIAL.
FT	TRANSMEM 153 173 POTENTIAL.
FT	TRANSMEM 217 237 POTENTIAL.
FT	TRANSMEM 276 296 POTENTIAL.
FT	TRANSMEM 308 328 POTENTIAL.
FT	TRANSMEM 344 364 POTENTIAL.
FT	TRANSMEM 384 404 POTENTIAL.
FT	TRANSMEM 408 428 POTENTIAL.
FT	TRANSMEM 441 461 POTENTIAL.
FT	TRANSMEM 472 492 POTENTIAL.
FT	TRANSMEM 549 569 POTENTIAL.
SO	SEQUENCE 615 AA; 68954 MW; B548FEC6E49326AD CRC64;

Db 224 AACLSSEFGGLIAGGCSKISGLKDMQYI-YIVEGICISLGFVFPYAFGLSKNLEDSWEPN 282
 QY 154 KPLYKYIAHHHHHNYKNTLSP-----FAGLAHPVD---GLQA 190
 Db 283 KEKEYISER---YKTNATDEPPEKEMFQWQAVKDKTWASAVALEGIDLTTEGLTFV 339
 QY 191 VPHYA-----LEFIPHTTHIGLFEAMWTANIH-----DCIGNIWM-- 230
 Db 340 LPIITSMGFTNRAQMLTPYIFLTAL-VFICAVMSDRKRLKSPFLACLTTSIGIA 398
 QY 231 PVNGAGYHTIHTTKYKNGHYTIMD-----WMFGS 262
 Db 399 IVLGSQVHGVR-----FGYIILCMGIYVNAACNMLSLSN 434

RESULT 14
 YRR6_MYCA STANDARD; PRT; 279 AA.
 AC P43045;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE HYPOTHETICAL 33.0 KDA PROTEIN IN LICA 3'REGION (ORF R6).
 OS Mycoplasma capricolum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 OC Entomoplasmatidae.
 NC NCBL_TaxID=2095;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 27343;
 RX MEDLINE=94051609; Pubmed=8233831;
 RA Miyata M., Sano K.-I., Okada R., Fukumura T.;
 RT "Mapping of replication initiation site in Mycoplasma capricolum
 genome by two-dimensional gel-electrophoretic analysis.";
 RL Nucleic Acids Res. 21:4816-4823(1993).
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 CC
 DR EMBL: D14982; BAA03623.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 279 AA; 33031 MW; D6D1A265B88D6C18 CRC64;

Query Match 5.8%; Score 90.5; DB 1; Length 279;
 Best Local Similarity 22.7%; Pred. No. 2.4; Mismatches 76; Indels 85; Gaps 14;
 Matches 38; Conservative 37;
 QY 52 LYFIS--GFLM-CFYIYVLKINVLPR-----DAIPFKAMRLQMFVAKA 94
 Db 26 LFLSLSLGFIETSYTDKLAIFEFKGFKEIYRWSIFDIIGTTELMFLEFNIMVL 85
 QY 95 M-PWYTLPLPVYSESMIRGWTGCFASIDFEGMILYFYAIALYVFEVGIWMHRELDHI 153
 Db 86 IESWFL--KSKTKKDNFMFK-----NMKMLKLYIYVYVYV--I 123
 QY 154 KPLKYL-----NATHHIYNKONTLSFAGLAHPV-----DG 186
 Db 124 KCIITTYKINADNGFGGADYILSSKYRNICILVSLVHICIGLENGEYIIHKFNKNDP 183
 QY 187 I-----LQAVPVIALFVPIHFTTHIGLFEAMWTANIHDCIHGNIW-PVNGAGY- 237
 Db 184 IYLDKXWIAQV--ILFIVILSYTIIYVLKGMTS--RPYYNIYIYDLDLKQVKNLGNH 238
 QY 238 ----HTIHTHTTKYKNGHYTIMD-----WMFGS 262
 Db 239 DMVDHYLNQSTFKHGF 254

RESULT 15
 COX3_MARPO STANDARD; PRT; 265 AA.
 ID COX3_MARPO
 AC P26858;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-JUN-1999 (Rel. 38, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE III (EC 1.9.3.1).
 GN COX3 OR COXIII.
 OS Marchantia polymorpha (Liverwort).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Marchantiophyta;
 OC Marchantiales; Marchantiaceae; Marchantia.
 NC NCBL_TaxID=3197;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92114051; Pubmed=1731062;
 RA Oda K., Yamato K., Ohta E., Nakamura Y., Takemura M., Nozato N.,
 RA Akashi K., Kanegae T., Ogura Y., Kohchi T., Ohyama K.;
 RT "Gene organization deduced from the complete sequence of liverwort
 Marchantia polymorpha mitochondrial DNA. A primitive form of plant
 mitochondrial genome.";
 RL J. Mol. Biol. 223:1-7(1992).
 CC -1- FUNCTION: SUBUNIT I, II, AND III FORM THE FUNCTIONAL CORE OF
 CC -1- THE ENZYME COMPLEX.
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O +
 CC 4 FERRICYTOCHROME C.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE SUBUNIT 3 FAMILY.
 CC
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 CC
 DR EMBL: M68929; AAC09434.1; -
 DR PIR: S25951; S25951.
 DR HSSP: P00415; 10CC.
 DR Mendel: 2057; MARPO; COX3.1.
 DR InterPro: IPR000298; Cytochrome_c.
 DR Pfam: PF00510; COX3.1.
 DR PROSITE: PS50253; COX3.1.
 KW Oxidoreductase; Mitochondrion; Transmembrane.
 SQ SEQUENCE 265 AA; 29595 MW; 43D1C7820C7E7BC CRC64;

Query Match 5.8%; Score 90; DB 1; Length 265;
 Best Local Similarity 23.1%; Pred. No. 2.5; Mismatches 53; Indels 62; Gaps 9;
 Matches 42; Conservative 25;
 QY 123 FGLIYEV-----YIATLVE-----VEFGIYWMHRELDIKPL-YKYLHA----- 162
 Db 84 YGIIIFVSEVMFLAFWAFHSSLAFTVEIGALWPKGSLVDPMGIPLNTIILISS 143
 QY 163 -----THHIYNKONTLSFAGLAHPVDGILLQAVPVIALFVPIHFTTHIGLFEAM 216
 Db 144 GAAVTWANH-----AIIAGLK-----QAAVYALIAVFLALVPTGFGGLEIYIAP 188
 QY 217 WTANIHDCIHGNIWPMVNGAGYHTI-----HTYKNGHYTIMDWM 258
 Db 189 FT--ISDGIYSTF-FLATGFHGFHVIIIGTIFLLICIGIRYLGHTTPKIHGFPAAPY 245
 QY 259 ME 260
 Db 246 HF 247

Mon Apr 8 17:54:19 2002

us-09-775-879-21.rsp

Page 10

Job time: 101 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 4, 2002, 17:05:57 ; Search time 16.4 Seconds
(without alignments)
1305.186 Million cell updates/sec

Title: US-09-775-879-21
Perfect score: 1562
Sequence: 1 MADNAYLMQFVDETSFYNR.....SLRDLLEDDNKRDSFKAE 281

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1538	98.5	281	2 S71251	C-5 sterol desatur
2	304.5	19.5	329	2 T40027	hypothetical c-5 s
3	295.5	18.5	365	2 J01146	C-5 sterol desatur
4	279.5	17.9	300	2 T37759	c-5 sterol desatur
5	174.5	11.2	286	2 T22444	hypothetical prote
6	167	10.7	253	2 G84695	probable C-4 stero
7	152.5	9.8	231	2 S76372	hypothetical prote
8	152.5	9.8	309	2 S64354	ERG25 protein - ye
9	149.5	9.6	258	2 B96718	probable sterol de
10	149	9.5	300	2 T16255	hypothetical prote
11	147.5	9.4	269	2 T22443	hypothetical prote
12	146	9.3	300	2 T38986	probable C-4 methy
13	138	8.8	303	2 T06618	hypothetical prote
14	129.5	8.3	258	2 A86277	hypothetical prote
15	127	8.1	820	2 T04570	hypothetical prote
16	122	7.8	255	2 T83409	hypothetical prote
17	117	7.5	293	2 T40740	hypothetical integ
18	117	7.4	349	2 S48533	SUR2 protein - yea
19	115.5	7.4	635	2 T02536	CER1-like protein
20	115	7.4	246	2 S74961	hypothetical prote
21	113	7.2	304	2 D82189	conserved hypothet
22	102.5	6.6	261	2 T12402	cytochrome-c oxida
23	99	6.3	493	2 T18789	hypothetical prote
24	98.5	6.3	301	2 G83556	hypothetical prote
25	98	6.3	615	2 S74277	probable membrane
26	98	6.3	615	2 S40624	probable membrane
27	94	6.0	555	2 T04146	glycosyl homolog -
28	93.5	6.0	386	2 S41691	ubiquinol--cytochr
29	93	6.0	936	2 B64567	cytochrome c bioge

30	92.5	5.9	542	2 B81662	apolipoprotein N-a
31	92.5	5.9	959	2 T25704	hypothetical prote
32	91	5.8	534	2 S64593	probable membrane
33	90.5	5.8	279	2 S42125	hypothetical prote
34	90	5.8	265	2 S25951	cytochrome-c oxida
35	90	5.8	318	1 S75765	stearoyl-CoA desat
36	89	5.7	351	2 T21004	hypothetical prote
37	89	5.7	373	2 G85355	nodulin-like prote
38	89	5.7	649	2 B38129	bo-type ubiquinol
39	88.5	5.7	308	2 S22928	ubiquinol--cytochr
40	88.5	5.7	353	2 T33974	hypothetical prote
41	88.5	5.7	1188	2 S48861	gene e1 protein -
42	88	5.6	321	2 A85970	probable transport
43	88	5.6	694	2 T12712	NADH dehydrogenase
44	88	5.6	694	2 T12675	NADH dehydrogenase
45	87.5	5.6	261	2 T11525	cytochrome-c oxida

ALIGNMENTS

```

RESULT 1
S71251
C-5 sterol desaturase (EC 1.-.-.-) - Arabidopsis thaliana
N:Alternate names: delta7-sterol-C5-desaturase; sterol-C5-desaturase
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 17-Mar-2000
C:Accession: S71251
R:Gachotte, D.; Husselstein, T.; Bard, M.; Benveniste, P.
submitted to the EMBL Data Library, July 1995
A:Description: Cloning a plant sterol-C5-desaturase by functional complementation of
A:Reference number: S71251
A:Accession: S71251
A:Molecule type: mRNA
A:Residues: 1-281 <GAC>
A:Cross-References: EMBL:X90454; NID:q1061037; PID:q106138
A:Superfamily: Saccharomyces cerevisiae ERG25 protein
C:Keywords: oxidoreductase

Query Match          98.5%; Score 1538; DB 2; Length 281;
Best Local Similarity 98.6%; Pred. No. 2,7e+128;
Matches 277; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 MADNAYLMQFVDETSFYNRIVSHLLPANLWEPRLPHLOTWLRNYAGTLVTFSGFLW 60
    |||||||
Db 1 MADNAYLMQFVDETSFYNRIVSHLLPANLWEPRLPHLOTWLRNYAGTLVTFSGFLW 60

OY 61 CFYIYVLTINVLPRKAIFPTIKAMRLQMFVAMKAMPWYTLPTVSE:MIERGWTGCFASI 120
    |||||
Db 61 CFYIYVLTINVLPRKAIFPTIKAMRLQMFVAMKAMPWYTLPTVSE:MIERGWTGCFASI 120

OY 121 DEFGWILYFVYIAYLVFEVFGIYWMHRELHDIKPLKYKYLHATNHT(NKONTLSPPAGLA 180
    |||||||
Db 121 GEGWILYFVYIAYLVFEVFGIYWMHRELHDIKPLKYKYLHATNHT(NKONTLSPPAGLA 180

OY 181 FHRVDSIIQAVPVIALFTVPIHFTTHIGLFEPAEATWTANIHCHISNIMPVAGAGYHTI 240
    |||||||
Db 181 FHRVDSIIQAVPVIALFTVPIHFTTHIGLFEPAEATWTANIHCHISNIMPVAGAGYHTI 240

OY 241 HHTYKHNKGHYTIWMDMFGSLRDLPLEDDNKRDSFKKAE 281
    |||||||
Db 241 HHTYKHNKGHYTIWMDMFGSLRDLPLEDDNKRDSFKKAE 281

RESULT 2
T40027
hypothetical c-5 sterol desaturase - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T40027
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Lauber, J.; Hilbert, H.; Duesterhoeft, A
submitted to the EMBL Data Library, December 1997

```

A:Reference number: Z21900
A:Accession: T40027
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-329 <WOO>
A:Cross-references: EMBL:AL021766; PIDN:CA16898.1; GSPDB:GN00067; SPDB:SPBC27B12.03c
A:Experimental source: strain 972h; cosmid c27B12
C:Genetics:
A:Gene: SPDB:SPBC27B12.03c
A:Map position: 2

[illegible]

RESULT 3
 J01146
 C-5 sterol desaturase (EC 1.-.-.-) - yeast (*Saccharomyces cerevisiae*)
 N.Alternate names: protein L2150; protein YLR056w
 C.Species: *Saccharomyces cerevisiae*
 C.Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 29-Oct-1999
 C.Accession: J01146 #S41993: S61630: S64884
 R.Arthington, B.A.; Bennett, L.G.; Skatrud, P.L.; Gynn, C.J.; Barbuch, R.J.; Ublright,
 Gene 102, 39-44, 1991
 A.Title: Cloning, disruption and sequence of the gene encoding yeast C-5 sterol desatura
 A.Reference number: J01146; MUID:91323727
 A.Accession: J01146
 A.Molecule type: DNA
 A.Residues: 1-365 <ART>
 A.Cross-references: EMBL:M62623; NID:g171474; PIDN:AAA34594.1; PID:g171475
 R.Renauld, G.; Lacroix, F.; Cassart, J.P.; Vandenhaute, J.; Delcour, J.
 submitted to the EMBL Data Library, March 1992
 A.Reference number: S41993
 A.Accession: S41993
 A.Molecule type: DNA
 A.Residues: 1-365 <REN>
 A.Cross-references: EMBL:M64989; NID:g171476; PIDN:AAA34595.1; PID:g171477
 R.Urristartazu, L.A.
 submitted to the EMBL Data Library, December 1995
 A.Reference number: S61618
 A.Accession: S61630
 A.Molecule type: DNA
 A.Residues: 1-365 <URR>
 A.Cross-references: EMBL:X94607; NID:g1181264; PIDN:CAA64303.1; PID:e217849; PID:g118127
 R.Andre, B.; Urristartazu, L.A.
 submitted to the Protein Sequence Database, May 1996
 A.Reference number: S64872
 A.Accession: S64884
 A.Molecule type: DNA
 A.Residues: 1-365 <AND>
 A.Cross-references: EMBL:273228; NID:g1360397; PIDN:CAA97586.1; PID:e245523; PID:g136039

A:Gene: SGD:ERG3; SYR1
A:Cross-references: SGD:S0004046; MIPS:YIR056w
A:Map position: 12R
C:Keywords: oxidoreductase; transmembrane protein
F:93-109/Domain: transmembrane #status predicted <TM1>
F:254-270/Domain: transmembrane #status predicted <TM2>

[illegible]

```

RESULT      4
T37759
c-5 sterol desaturase - fission yeast (Schizosaccharomyces pombe)
C.Species: Schizosaccharomyces pombe
C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #tex_change 03-Dec-1999
C.Accession: T37759
R.Wedter, H.; Wambolt, R.; Wood, V.; Rajadream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, December 1998
A.Reference number: Z21744
A.Accession: T37759
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-300 <MED>
A.Cross-references: EMBL:AL035064; PIDN:CAA22610.1; GSPDB:GN00066; SPDB:SPAC1687.16c
A.Experimental source: strain 97Zh; cosmid c1687
C.Genetics:
A.Gene: SPDB:SPAC1687.16c
A.Map position: 1

Query Match          17.9%; Score 279.5; DB 2; Length 300;
Best Local Similarity 27.6%; Pred. No. 2, 5e-17;
Matches 76; Conservative 53; Mismatches 107; Indels 39; Gaps 11;

QY    7 YLMQEVDE---TSFNRIYLSHLPLANL-WERLPNHLQTLWLNRYLAGTLTYFTSGFLKCF 62
      || : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     3 YLLNVADQYALDSIYNVAV--PLARDNIVRQSISLEFLTW---FCGMFLYLTFASLSYO 56
      :: | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY    63 YIY-----YLKINVLPPKDAIPTIKAMRLQMVAKKAMPWTLLPVTSSMLE-RG 112
      :: | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     57 FVFEDSLMDHPKFLKNQV-----MEVTLALQNLPGMALL-TVPMFLAEIRG 102
      :: | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY    113 IWRKCFASIDFQGLILFFVYIAIYLFVEFGIWMHRELDIKLYUYUATHTNYKONT 172
      :: | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     103 YSLVDNISDYGLKTYFLCSLPWFMSDFGIYWAHRFLNH-RIVYPRLRKLHH---KWII 158
      :: | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY    173 LSPFAGLAHPVDGILQAAPHVIALFIPIVPHFTTHGLFMEAINTANIHDICIGNIWPY 232

```

Db 159 CTPYASHAFKSGADGFLQSLPYHLFPFPPLKFLYLAFTFEVNFWSIMIHOCKYISNNPI 218
 Oy 233 M-GAGYHTIIHHTTYKHNHGYHTIMDMMGSLRDP 266
 Db 219 INGAHHNGHHIYFENVYNGQFTTFLDLGNSFRAP 253

RESULT 5

T22444

hypothetical protein F49E12.10 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000

C:Accession: T22444

R:Thomas, K.

Submitted to the EMBL Data Library, October 1995

A:Reference number: Z19565

A:Accession: T22444

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-286 <WIL>

A:Cross-references: EMBL:Z66520; PIDD:CA91384.1; GSPDB:GN00020; CESP:F49E12.10

A:Experimental source: clone F49E12

C:Genetics:

A:Gene: CESP:F49E12.10

A:Map position: 2

A:Introns: 21/2; 130/2; 153/1; 221/2

C:Superfamily: Saccharomyces cerevisiae ERG25 protein

Query Match 11.2%; Score 174.5; DB 2; Length 286;
 Best Local Similarity 22.4%; Pred. No. 4.3e-08;
 Matches 64; Conservative 49; Mismatches 112; Indels 61; Gaps 14;

Oy 39 LQTLRLNLAFT--LLYFISG-----FLKCFYIYLLKINVYLPKDAIPTKAMRLQMFV 90
 Db 5 LYRLKYNFDEDEYMLVYVAVANAGISFWLNFIIIDVDPK---WQPKYIOEEK 60
 Oy 91 AMKAMPWTLLPTVSESM-----IERGWTCKFASIDFGMTLVYVYIAIYLV 137
 Db 61 KPSISKYISILKVVGPNOILYTPYITVTLMEYVARMWGMDFGVIP-SWITILRLDACLCA 119
 Oy 138 FVEGIVMARELDIKPLKYULNATHNIYKONTLSFPAIGLAFHPVDGILQAVPHVIAL 197
 Db 120 MDEIGFYTHRLFHNPK-LYKHKKHHEMNAPVIS---SIYAPLE--HAISNLSP 172
 Oy 198 FIVYIHFTTHI---GLFMEAIWTANIHDCIHGNTWPM-GAGYHTIIHHTTYKHNHGYHT 253
 Db 173 YLGAVLFCHVSHYIFTSVAIILTTFHH--SGYHFPMLSAEHDFHKKVFNCCYGGP 230
 Oy 254 IWMDMMG-----SLRDP-----LLEEDONKDSFCK 279
 Db 231 --LWMLHGTDTFKRSIHPNDYVYGGTTPIKELIPEDKNNNKK 274

RESULT 6

G84695

probable C-4 sterol methyl oxidase [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C:Accession: G84695

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffett, K.S.; Crokin, L.A.; Shen, M.; Vankam, S.E.; Umayam, L.; Tallon, L.;

euse, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402:761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487

A:Accession: G84695

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-253 <STO>

A:Cross-references: GB:AE002093; NID:g3980396; PIDD:MAC95199.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g29390
 A:Map position: 2

Query Match 10.7%; Score 167; DB 2; Length 253;
 Best Local Similarity 22.2%; Pred. No. 1.7e-07;
 Matches 58; Conservative 32; Mismatches 75; Indels 96; Gaps 11;

Oy 52 LYFISGLMCF-----YIYLLKINVYLPKDAIPTK 82
 Db 26 VEFSLPRTFIERGELSNIYKIQTKSNTPPEAGKCIARLLHCCVNLPLMASYPVFR 85
 Oy 83 ARRLQFVAMKAMPWTLLPTVSESMIERGWKCFASIDFGMTLVYVYIAIYLVVERG 142
 Db 86 FMGME-----SSFP-----LPS-----WKVVS/QILFYFIIDRY 115
 Oy 143 IYWMARELDIKPLKYULNATHNIYKONTLSFPA-----GLAFHPVDGILQ 190
 Db 116 FYWGRHILH-TKWLKYNVSHVHEX-----AFPEGLTSEVAPHAELILGFAITVGPALT 169
 Oy 191 VPHVIALFVPIHFTTHIGLMEAIWTANIHDCIH-----GNIWYVH-GAGYHTIIHHT- 243
 Db 170 GHLLITLWL-----WMLRVLETVEAHGCGYHFPWSPSNFLPL:GGADPHDYHNR 219
 Oy 244 --TYKHNHGYHTIWMDMFGS 262
 Db 220 LYTKSGNYSSTFYVMDMIRGT 240

RESULT 7

S76372

hypothetical protein - Synechocystis sp. (strain PCC 6803)

C:Species: Synechocystis sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999

C:Accession: S76372

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys

s.

A:Reference number: S74322; MUID:97061201

A:Accession: S76372

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-231 <KAN>

A:Cross-references: EMBL:D64000; GB:AB001339; NID:g1001464; PIDD:BA10224.1; PIDD:d101

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 9.8%; Score 152.5; DB 2; Length 231;
 Best Local Similarity 23.6%; Pred. No. 3e-06;
 Matches 58; Conservative 42; Mismatches 113; Indels 33; Gaps 9;

Oy 23 LSHLLPANLMEPLPHLQTLNRYL---AGTLTYFISGLMCFYIYLLKINVYLPKDAIP 79
 Db 1 MDHL-----FWIYLVFFAILRLFRYLACGTAFYFSPGOSILKNHLPLN-----IP 49
 Oy 80 TKAMRLQFVAMKAMPWTLLPTVSESMIERGWKCFASIDFG--NIIYVYIAIYLVF 138
 Db 50 SSQSIKDKILKLSIISAIIPALAGAFILSSYGKMNLYVDPOHGNVIGISVLI-LFL 108
 Oy 139 VEFQIVMARELDIKPLKYULNATHNIYKONTLSFPAIGLAFHPVDGILQAVPHVIALF 198
 Db 109 QDLYEYFTHRLFHNPR-LFSLFHKGNHLSRYPLTFSF--AFDLPZALVQSFLLIYVS 164
 Oy 199 IYPIHFTTHIGLMEAIWTANIHDCIH-----GNIWYVH-GAGYHTIIHHTYKH 247
 Db 165 LIRLHFTTILALIMKTIMSVINHLCIDRLPLAFPHIMLGKVF--ITVAHSHLHLKYNA 222
 Oy 248 NNGHYT 253
 Db 223 NYGLYS 228

```

RESULT      8
S64354
ERG25 protein - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein G4358; protein YGR060w
C:Species: Saccharomyces cerevisiae
C:Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 20-Jun-2000
C:Accession: S64354
R:Entian, K.D.; Rose, M.; Koetter, P.; Roehmer, A.; Sehnsam, I.; Hempel, S.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64335
A:Accession: S64354
A:Molecule type: DNA
A:Residues: 1-309 <ENT>
A:Cross-references: EMBL:z72845; NID:g1323076; PIDN:CAA97062.1; PID:g1323077; MIPS:YGR060
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:ERG25
A:Cross-references: SGD:S0003292; MIPS:YGR060w
A:Map position: 7R
C:Superfamily: Saccharomyces cerevisiae ERG25 protein
C:Keywords: transmembrane protein
C:151-67/Domain: transmembrane #status predicted <TM>

```

Db 179 HLHPELFVVGTFITITP-----WIFPHCLTYWIMFIAOSVSEVHIGDPEPALMRI 233
Oy 229 IMPVAGAGYHTIHH 242
| | | | |
Db 234 FWFYSGARAHDMNH 247

RESULT 11
T22443
hypothetical protein F49E12.9 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Jun-2000
C:Accession: T22443
R:Thomas, K.
submitted to the EMBL Data Library, October 1995
A:Reference number: Z19565
A:Accession: T22443
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-269 <WLL>
A:Cross-references: EMBL:Z66520; PIDN:CAA91383.1; GSPDB:GN00020; CESP:F49E12.9
A:Experimental source: clone F49E12
C:Genetics:
A:Gene: CESP:F49E12.9
A:Map position: 2
A:introns: 20/2; 129/2; 152/1; 174/1; 202/1; 220/2
C:Superfamily: Saccharomyces cerevisiae ERG25 protein

Query Match 9.4%; Score 147.5; DB 2; Length 269;
Best Local Similarity 23.2%; Pred. No. 9.7e-06;
Matches 55; Conservative 40; Mismatches 99; Indels 43; Gaps 11;

Oy 51 LLYFISGL-----WCYIYYLKINLYLPKDAIP-----TIKAMRLQM 88
| | | | | : : : : :
Db 18 LLYVGGVIVININWLELFFITIDMDPKWQPYKIODEKRPPLSKYLGAFKYLANO 77
| | | | | : : : : :
Oy 89 FVAMKAMPWYTLPTVSESMIERGW-TKCFASIDEFGWILYVYAIYLVFVEFGIYMH 147
| | | | | : : : : :
Db 78 FIAGLILILFWYFAY-----WFGTSFTCPRLPSGMQI-FRDIVISILCEIGFYISH 128
| | | | | : : : : :
Oy 148 RELHDIKPLVYUHLATNHIYKNTLSPFAGLAFHPVDGILQAVPHVIALFTVPIHFTTH 207
| | | | | : : : : :
Db 129 RLFIHPK-IYKYIKHKHHEWAPVIT---SIYCHPLE---HAISNLSVLLGPTICGSH 181
| | | | | : : : : :
Oy 208 IGLFMEAIWIANIHDCIH-GNIWPVM-GAGYHTIHTTITKINIGHYTTIMMMMGCS 262
| | | | | : : : : :
Db 182 VITLWIASIALISTTCSHSGYHFPFMLSPEPHDYHKKVNECFG--TGLLDIMHGT 236
| | | | | : : : : :

RESULT 12
T38986
probable c-4 methyl sterol oxidase - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C:Accession: T38986
R:McDonnell, R.C.; Rajandream, M.A.; Barrell, B.G.; Zimmermann, W.; Wambutt, R.
submitted to the EMBL Data Library, August 1999
A:Reference number: Z21822
A:Accession: T38986
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-300 <MCD>
A:Cross-references: EMBL:ALJ09832; PIDN:CA852730.1; GSPDB:GN00066; SPDB:SPAC630.08c
A:Experimental source: strain 972h-; cosmid c630
C:Genetics:
A:Gene: SPDB:SPAC630.08c
A:Map position: 1
C:Superfamily: Saccharomyces cerevisiae ERG25 protein

Query Match 9.3%; Score 146; DB 2; Length 300;
Best Local Similarity 23.6%; Pred. No. 1.5e-05;

Matches 73; Conservative 41; Mismatches 113; Indels 82; Gaps 19;
Oy 8 LMQFVDETFYRIVYLSHLPLANLMEPLPHLOQTWIRNYIAGTLFLFISGLMCEFIYYL 67
| | | | | : : : : :
Db 20 LQMPHELNFVEQLMLAY-----YKMFDDNDVAVAGL--MSFLHLELITFG 62
| | | | | : : : : :
Oy 68 KINVLPKDAIPITIKAMRLQ-MEVAMKAMPW-YTLPTVSESMIE--RGM---TKC---- 116
| | | | | : : : : :
Db 63 RCIPWMIIDAMPYFRWKIQPKKVPFLAEQWECTRLVLSHFLVELPQIWLPRMCAITG 122
| | | | | : : : : :
Oy 117 -----FASIDEGWILYVYAIYLVVEFGIYMHRELHDIKPLKYKYLATNHIYKNO 170
| | | | | : : : : :
Db 123 LSTSVFPPPVTKMIW-----QITLFFELDTWYHMAHLFPH-YGIFYFFIHKVNHRSY-- 174
| | | | | : : : : :
Oy 171 NTLSPFAGLA---FHPVDGILQA-----VPHVIALFTVPIHFTT---IGLLEMEAI--- 216
| | | | | : : : : :
Db 175 ---APF-GLSAEYANPLETEILGAGTVFVPLMKCYTTHDLVATKYIVITLRLQVDSH 230
| | | | | : : : : :
Oy 217 -----WTANIHDCIHGNIMPV-MGAGYHTIHTTITKINIGHYTTIMMFMGSLRPLLE 269
| | | | | : : : : :
Db 231 AGYDFPWSLN-----KFLPIWAGADHHDIYHMAKNDPSSSFRM--W-----DAVLK 275
| | | | | : : : : :
Oy 270 EDDNKDSFK 278
| | | | | : : : : :
Db 276 TDQNVHQFK 284
| | | | | : : : : :

RESULT 13
T06618
hypothetical protein F16J13.180 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 10-Dec-1999
R:Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancro
submitted to the Protein Sequence Database, April 1999
A:Reference number: Z15789
A:Accession: T06618
A:Molecule type: DNA
A:Residues: 1-303 <BEV>
A:Cross-references: EMBL:AL049638; GSPDB:GN00062; ATSP:F16J13.180
A:Experimental source: cultivar Columbia; BAC clone F16J13
C:Genetics:
A:Gene: ATSP:F16J13.180
A:Map position: 4
A:introns: 112/3; 220/2; 269/3; 285/3
C:Superfamily: Saccharomyces cerevisiae ERG25 protein

Query Match 8.8%; Score 138; DB 2; Length 303;
Best Local Similarity 23.5%; Pred. No. 7.6e-05;
Matches 52; Conservative 33; Mismatches 72; Indels 64; Gaps 11;

Oy 86 LQNFVAMKAMPWYTLPTVSESMIERGWTKCFASIDEFGWILYVYAIYLVFVEGIYW 145
| | | | | : : : : :
Db 111 IOMIEIRSLP---LPTITMELSQ-----LVVFLIEDTYTNW 145
| | | | | : : : : :
Oy 146 MRELDIKPLKYUHLATNHIYKNO-NTLSFPFAGLAFHPVDGILQAVPHVIALFTVPIH 204
| | | | | : : : : :
Db 146 VHRFFHS-KWGDYKIRHVNHEYTAPIGYAPYA---HMAEVLILLIPYFMGPAIAPGH 200
| | | | | : : : : :
Oy 205 TTH---IGLLEMEAI-----WTANIHDCIHGNIMPVMGAGYHTIHTT---TKNHV 249
| | | | | : : : : :
Db 201 ITFWLMIALRQMEAITHTSGYDEPRWPTKYIPRYG-----GAEYHLYHHYVGGOSQSNF 254
| | | | | : : : : :
Oy 250 GHYTTIMMMMGCS-----LRDPLLEDDNKDSFKFA 280
| | | | | : : : : :
Db 255 ASVFTYCDYIYGTDKMMLQGYRFOKKLLEQ--IKSSSKS 293
| | | | | : : : : :

RESULT 14
A86277
hypothetical protein AAF43928.1 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2002, 17:05:32 ; Search time 12.63 Seconds

(without alignments)
500.667 Million cell updates/sec

Title: US-09-775-879-21

Perfect score: 1562

Sequence: 1 MAADNAYLMQFVDETSFYNR.....SLRDLLEDDNKDSFKAE 281

Scoring table:

BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCUTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	135.5	8.7	625	US-08-581-148C-18	Sequence 18, Appl
2	104.5	6.7	594	US-08-581-148C-16	Sequence 14, Appl
3	98	6.3	555	US-08-581-148C-14	Sequence 16, Appl
4	90	5.8	318	US-08-309-182B-3	Sequence 3, Appl
5	85	5.4	407	US-08-742-440A-3	Sequence 3, Appl
6	81	5.2	1732	US-08-477-451-14	Sequence 14, Appl
7	81	5.2	2713	PCR-US96-01735-1	Sequence 1, Appl
8	80.5	5.2	408	US-08-742-440A-6	Sequence 6, Appl
9	80	5.1	360	US-08-597-236-11	Sequence 11, Appl
10	80	5.1	360	US-08-746-682A-11	Sequence 11, Appl
11	76.5	4.9	325	US-08-467-948A-29	Sequence 29, Appl
12	76.5	4.9	325	US-08-467-947A-29	Sequence 29, Appl
13	76.5	4.9	338	US-08-988-876-8	Sequence 8, Appl
14	76.5	4.9	439	US-09-303-524A-2	Sequence 2, Appl
15	76.5	4.9	439	US-08-716-873-4	Sequence 4, Appl
16	76.5	4.9	439	US-09-368-431-4	Sequence 4, Appl
17	75.5	4.8	355	US-08-461-244-2	Sequence 2, Appl
18	75.5	4.8	355	US-09-045-583-56	Sequence 56, Appl
19	75.5	4.8	362	US-08-902-853-5	Sequence 5, Appl
20	75.5	4.8	380	US-08-244-205-11	Sequence 11, Appl
21	75.5	4.8	380	US-08-244-205-2	Sequence 11, Appl
22	75.5	4.8	386	PCR-US92-10284-11	Sequence 2, Appl
23	75.5	4.8	386	PCR-US92-10284-2	Sequence 2, Appl
24	75.5	4.8	1581	US-08-726-320-3	Sequence 3, Appl
25	75.5	4.8	1581	US-09-208-716-3	Sequence 3, Appl
26	75	4.8	438	US-08-952-365-2	Sequence 2, Appl
27	75	4.8	3165	US-08-459-146-3	Sequence 3, Appl

28	75	4.8	3165	US-08-459-065-3	Sequence 3, Appl
29	75	4.8	3287	US-08-477-451-7	Sequence 7, Appl
30	74	4.7	261	US-09-097-889-19	Sequence 19, Appl
31	73.5	4.7	439	US-08-716-873-2	Sequence 2, Appl
32	73.5	4.7	439	US-09-368-431-2	Sequence 2, Appl
33	73.5	4.7	479	US-08-484-105-10	Sequence 10, Appl
34	73.5	4.7	479	US-08-484-106-10	Sequence 10, Appl
35	73	4.7	474	US-08-453-742-2	Sequence 2, Appl
36	73	4.7	474	US-08-454-464-2	Sequence 2, Appl
37	73	4.7	474	US-08-453-222-2	Sequence 2, Appl
38	73	4.7	474	US-08-452-802-2	Sequence 2, Appl
39	73	4.7	477	US-08-453-742-27	Sequence 27, Appl
40	73	4.7	477	US-08-454-464-27	Sequence 27, Appl
41	73	4.7	477	US-08-453-222-27	Sequence 27, Appl
42	73	4.7	477	US-08-452-802-27	Sequence 27, Appl
43	72.5	4.6	1498	US-08-404-531B-28	Sequence 28, Appl
44	72.5	4.6	1498	US-08-404-531B-29	Sequence 29, Appl
45	72.5	4.6	1498	US-08-476-900A-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-08-581-148C-18
: Sequence 18, Application US/08581148C
: Patent No. 6060644
: GENERAL INFORMATION:
: APPLICANT: Schnable, Patrick S.
: APPLICANT: Robertson, Donald S.
: APPLICANT: Hansen, Joel D.
: APPLICANT: Nikolau, Basil J.
: APPLICANT: Xu, Xiaojie
: APPLICANT: Xia, Yijl
: TITLE OF INVENTION: ISOLATION AND USE OF CUTICULAR LIPID
: TITLE OF INVENTION: GENES
: NUMBER OF SEQUENCES: 30
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Leydig, Volt & Mayer, Ltd.
: STREET: Two Prudential Plaza, Suite 4900
: CITY: Chicago
: STATE: IL
: COUNTRY: US
: ZIP: 60601-6780
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/581,148C
: FILING DATE: 29-DEC-1995
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: Larcher, Carol
: REGISTRATION NUMBER: 35243
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 616-5600
: TELEFAX: (312) 616-5700
: INFORMATION FOR SEQ ID NO: 18:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 625 amino acids
: TYPE: amino acid
: TOPOLOGY: unknown
: MOLECULE TYPE: protein
: US-08-581-148C-18

Query Match 8.7%; Score 135.5; DB 3; Length 625;
Best Local Similarity 22.8%; Pred. No. 6.5e-07;
Matches 55; Conservative 34; Mismatches 71; Indels 81; Gaps 11;

QY 64 IYIKINIVYLPKDAIPITKAMRLQMEVAMKAMPYTLPTVSESNIEGKTCFASIDEF 123
DB 105 LEYIGIN-----LAEKGQLPWMRTDGVLMGALIHFG----- 136
QY 124 GWILYFYVIAIYLVFEGGIYMMHRELHDIKPKLYLHATHH--IYNQNT--LSFAGL 179
DB 137 -----PVEFLYVWKALHH-HFLYSRYSHSHSSIVTEPTISVHPFAE- 180
QY 180 AFHPVDGILQAVPHVIAL-----FIVPIHFTTHIGLFEAIAWTANIHCING 227
DB 181 --HIAVFILFALPLTLTLVTKASISFAGYIYIDFNMMNHCNFEILPKRLH----- 233
QY 228 NIMVVM-----GAGYHITHHTTKYKNGHYIIMDMFGSL---RDLLEE-----DDNK 274
DB 234 -LFPPLKFLCYTPSYSHLHOFRTNYSLFMPLYDIYGTDESDITLVEKTLERGDDRV 292
QY 275 D 275
DB 293 D 293

RESULT 2
US-08-581-148C-14
; Sequence 14, Application US/08581148C
; Patent No. 6060644
; GENERAL INFORMATION:
; APPLICANT: Schnable, Patrick S.
; APPLICANT: Robertson, Donald S.
; APPLICANT: Hansen, Joel D.
; APPLICANT: Nikolau, Basil J.
; APPLICANT: Xu, Xiaojie
; APPLICANT: Xia, Yijl
; TITLE OF INVENTION: ISOLATION AND USE OF CURRICULAR LIPID
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Volt & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: US
; ZIP: 60601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/581,148C
; FILING DATE: 29-DEC-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Larcher, Carol
; REGISTRATION NUMBER: 35243
; REFERENCE/DOCKET NUMBER: 71380
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 594 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-581-148C-14

Query Match 6.7%; Score 104.5; DB 3; Length 594;
Best Local Similarity 19.0%; Pred. No. 0.0021;
Matches 52; Conservative 34; Mismatches 74; Indels 113; Gaps 12;
QY 60 WCFIYI--YIKINIVYLPKDAIPITKAMRLQMEVAMKAMPYTLPTVSESNIEG 111
DB 60 WCFIYI--YIKINIVYLPKDAIPITKAMRLQMEVAMKAMPYTLPTVSESNIEG 111

DB 9 WCFHILVISLRFNLVM-----WYINICMMLFLTRNRRLHQ 45
QY 112 GWKCFASID-EFGMIYFYV-----IAIYLVFVERG----- 142
DB 46 SID--FNQIDKEMWMDNVIQALIASIATIMFQEFANLPVWKTKGLVAIVYHVYSE 103
QY 143 --IYMMHRELHDIKPKLYLHATHIYNKNTLSFAGLAHPVDGILQAVPHVIALFIV 200
DB 104 PLYWVILRLHT-----NYLTPYH-----SFHSSAVQPVYVGSSTFLE 144
QY 201 PIHFTTHIGL-----FMEAIWTANIHCING--NIMP----- 231
DB 145 ELLVAVGLPILCCSLSGSKSIYGYLVDFPLRCGLGHSNVEIMPHWIEFYFFPFRF 204
QY 232 -VMGAGYHITHHTTKYKNGHYIIMDMFGSL 263
DB 205 IITYPTIYSLHSEKSNVCLFMPLYDTMNTL 237

RESULT 3
US-08-581-148C-16
; Sequence 16, Application US/08581148C
; Patent No. 6060644
; GENERAL INFORMATION:
; APPLICANT: Schnable, Patrick S.
; APPLICANT: Robertson, Donald S.
; APPLICANT: Hansen, Joel D.
; APPLICANT: Nikolau, Basil J.
; APPLICANT: Xu, Xiaojie
; APPLICANT: Xia, Yijl
; TITLE OF INVENTION: ISOLATION AND USE OF CURRICULAR LIPID
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Volt & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: US
; ZIP: 60601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/581,148C
; FILING DATE: 29-DEC-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Larcher, Carol
; REGISTRATION NUMBER: 35243
; REFERENCE/DOCKET NUMBER: 71380
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 555 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-581-148C-16

Query Match 6.3%; Score 98; DB 3; Length 555;
Best Local Similarity 21.5%; Pred. No. 0.01;
Matches 39; Conservative 27; Mismatches 59; Indels 56; Gaps 9;
QY 114 TKCFASIDEFGMIYFYVIAIYLVFEGGIYMMHRELHDIKPKLYLHATHIYNKNTL 173
DB 50 TSDSLAMDRLGMA--IAVVLHVAVSEPAFYWAHRAH-LGRLFSRYSHSHSFOATQAL 105

OY 174 SPFAGLAFHPVDGI---LQAVPHVIALFIVPIHFTTHIGLMEAIWTANIDCHIGNI- 229
Db 106 T--AGFV--TPLESLLTLIVAMPHLOGL-----HGG-----TRLRELIVYGHIS 144
OY 230 ---WPMCA-----GHTTHHTTYKINYGHTIWMDMRGS 262
Db 145 SSTFVHGVOORGHJLQDFODFPLRYLIYTPSYLSLHREKDSNFCIFMPLFALGCT 204
OY 263 L 263
Db 205 L 205

RESULT 4

US-08-309-182B-3
; Sequence 3, Application US/08309182B
; Patent No. 5639645
; GENERAL INFORMATION:
; APPLICANT: No. 563964510 MURATA
; TITLE OF INVENTION: A RECOMBINANT 9 DESATURASE AND A GENE
; TITLE OF INVENTION: ENCODING THE SAME
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/309,182B
; FILING DATE: September 20, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 318 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-309-182B-3

Query Match 5.8%; Score 90; DB 1; Length 318;
Best Local Similarity 19.0%; Pred. No. 0.039;
Matches 55; Conservative 38; Mismatches 117; Indels 80; Gaps 10;

OY 42 WIRNYLACTLVFISGFLMCFYIYLYIKINVLPKDAIPTIK-----AM 84
Db 11 YLSKLFDSLSLYFNKROLFRFVRFPMFALPNDSPKPLTPAWVIEFFTSIHVALLA 70
OY 85 RLOMVAKAMPWYTLPLPVSESM--IERGWTGCPA--SIDEQWILYFYIAIYL----- 136
Db 71 FLPOFFSMKAVGMAFLLYVIGGIGITLGGFHRCSHRSFNVPKMLEYLFVIGCTLACOGG 130
OY 137 VFERGIYWMHRELHDIPLYKYLLHATHIYK----- 169

Db 131 VEWVGLRHHMKFSDDTP-----DPHDSNKGFWMSHIGMMFEIPAKADIPRYTKDI 183
OY 170 -----QNTL-----SPFAGLAFHPVDSILQAVPHVIALFIVPIHFTTHIGLMEAIW 217
Db 184 QDDKRYQCCNNLLILIOVALGLILFALGWPVIVGIFVRLVFEHFTVEVNSATHKFGY 243
OY 218 TANIHDCIHGINIPV-----MGAGYHTIHTTYKHNHNGHTIW-----MDYM 259
Db 244 VSHESNDYSRNCMWVALLTFGEGWNNHH-AVOYSARHOLQWMEVDLTMM 292

RESULT 5

US-08-742-440A-3
; Sequence 3, Application US/08742440A
; Patent No. 5892014
; GENERAL INFORMATION:
; APPLICANT: Coughlin, Shaun
; APPLICANT: Ishihara, Hiroaki
; APPLICANT: Connolly, Andrew
; TITLE OF INVENTION: Protease Activated Receptor
; TITLE OF INVENTION: 3 and Uses thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Bozicevic & Reed, LLP
; STREET: 285 Hamilton Avenue, Suite 200
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,440A
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: UCAL/060PAT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-327-3400
; TELEFAX: 650 327-3231
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 407 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; US-08-742-440A-3

Query Match 5.4%; Score 85; DB 2; Length 407;
Best Local Similarity 23.7%; Pred. No. 0.2;
Matches 59; Conservative 33; Mismatches 85; Indels 72; Gaps 15;

OY 51 LLYFISGFLMCFYIYLYIKI-----NVLPRDAIPTIKAMRLOMFVAKAMPWYTLAPT 103
Db 165 IAYHLNGNNWVGEWMCRTTVVFGNMYC---AIIILTCMGINRFLATAHFTYQKLPK 221
OY 104 VESMERGTWTCFASIDEFGWILYFYIAIYLVFVSEGIYMMHREL---HDIKPLKYLL 160
Db 222 RSFSILMCG-----IYMWVFLYMLPEVILKO-EYHLVSHSITTCYCHDVVACESP 270
OY 161 HATHHIYNKNTLSPFAGLAFHPVDSILQAVPHVIALFIVPIHFTTHI-GLLMEAIWTA 219

DB 271 SSREFY-----FVSLAF---GFL--IPEVITFC---YTLIHKKSKDRIMLG 313
QY 220 NIHDCI-----HGNIMPMGAGYHTIHTTQYKHNHYTIMDMWF-----GS 262
DB 314 YIRAVLLIVFTICAFPTNIIIV-----IHMANI---YHNHTDSLRYMILALCLGS 363
QY 263 LR--DPL 268
DB 364 LNSCLDPFL 372

RESULT 6

US-08-477-451-14
; Sequence 14, Application US/08477451
; Patent No. 5928865
; GENERAL INFORMATION:
; APPLICANT: Covacci, Antonello
; TITLE OF INVENTION: Helicobacter Pylori Cagl Region
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,451
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McClung, Barbara G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0335.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-601-2708
; TELEFAX: 510-655-3542
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1732 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-477-451-14

Query Match Best Local Similarity 5.2%; Score 81; DB 2; Length 1732;

Matches 43; Conservative 23; Mismatches 96; Indels 62; Gaps 7;

QY 75 KDAIPITKARLQMFVAMKAMPWYTLPTVSESMIERGWTGCFASIDFQWILYFYIAI 134
DB 1113 KAIPIPTKAIKDHCMIFLR-----RAMISNLMDLFLFLIIMIAIFHH--- 1157
QY 135 YLVFVEGIGIWMHRELHDIPRYKYLH-----ATHIYINKONTLSPPAGLAFHPVDGI 187
DB 1158 ERCEFLVEDRWAVARISDCLMLYLLHFLLYOCOTRLHLPVGSYFLAPFLFFSSHKRTKL 1217
QY 188 LQAVPHVIALFVIPHTTHIGL-----LMEAI-----WTANIHDC 224
DB 1218 ER-----FYCCCEYVLNHLGVVKTCTYFLSLFLEFFLINGQEFFDPCLSNFTLTHNRC 1270
QY 225 IHGNIMPMGAGYH-----TIHTTQYKHNHYGHTTIMDMW 258
DB 1271 LKTYTHFOFAFSTHQNAEQOVSKIHSPSSHSYHLYITMFW 1314

RESULT 7

PCT-US96-01735-1
; Sequence 1, Application PC/TUS9601735
; GENERAL INFORMATION:
; APPLICANT: Marks, Andrew R.
; TITLE OF INVENTION: HUMAN T CELL INOSITOL 1,4,5,-TRISPHOSPHATE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/01735
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/386,039
; FILING DATE: 09-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KOLE, Lisa B
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: A30042 - 165/30555
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-408-2628
; TELEFAX: 212-765-2519

QY 9 MQEVDETSFYNRIVLSHLRANIMEPLRPHLQTWLRNYLAGTLLYTSGLMCFYIYK 68
DB 2234 MSFWSISIF-NLAVMLNLVAFIYP-----LKGVRGRTGLRPHMSGLTMGLISLG 2283
QY 69 INVYLPK--DAIPITKARLQMFVAMKAMPWYTLPTVSESMI-----ERG 112
DB 2284 IVIGLPHNPGIRALIGSTIRLIFSVGSOPALFLGAFNVCNKIIFLMSFVNGCGFTTNG 2343
QY 113 WTKCFASIDFQWILYFYIAIYLVFVEGIGIWMHRELHDIPRYKYLHATHIYINKONT 172
DB 2344 YRANVVLVD-----VELYHLLIVYICAKGLF-----VHVFYSLLLDLVYRESL 2390
QY 173 LSPFAGLAFHPVDGIQAVPHVIALFTVPIHTTHIGLME 214
DB 2391 LNVIAKSVTRNGRSIITLAVLALLIVLYFSI-----VGYLFFK 2427

Query Match Best Local Similarity 5.2%; Score 81; DB 5; Length 2713;

Matches 51; Conservative 34; Mismatches 93; Indels 44; Gaps 8;

QY 2234 MSFWSISIF-NLAVMLNLVAFIYP-----LKGVRGRTGLRPHMSGLTMGLISLG 2283
QY 69 INVYLPK--DAIPITKARLQMFVAMKAMPWYTLPTVSESMI-----ERG 112
DB 2284 IVIGLPHNPGIRALIGSTIRLIFSVGSOPALFLGAFNVCNKIIFLMSFVNGCGFTTNG 2343
QY 113 WTKCFASIDFQWILYFYIAIYLVFVEGIGIWMHRELHDIPRYKYLHATHIYINKONT 172
DB 2344 YRANVVLVD-----VELYHLLIVYICAKGLF-----VHVFYSLLLDLVYRESL 2390
QY 173 LSPFAGLAFHPVDGIQAVPHVIALFTVPIHTTHIGLME 214
DB 2391 LNVIAKSVTRNGRSIITLAVLALLIVLYFSI-----VGYLFFK 2427

RESULT 8

US-08-742-440A-6

; Sequence 6, Application US/08742440A

; Patent No. 5892014

; GENERAL INFORMATION:

; APPLICANT: Coughlin, Shaun

; APPLICANT: Ishihara, Hiroaki

; TITLE OF INVENTION: Protease Activated Receptor

; TITLE OF INVENTION: 3 and Uses thereof

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Bozicevic & Reed, LLP

; STREET: 285 Hamilton Avenue, Suite 200

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/742,440A

; FILING DATE: 30-OCT-1996

; CLASSIFICATION: 536

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Sherwood, Pamela J

; REGISTRATION NUMBER: 36,677

; REFERENCE/DOCKET NUMBER: UCAL/060PAT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-327-3400

; TELEFAX: 650-327-3231

; TELETYPE:

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 408 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; FEATURE:

; US-08-742-440A-6

Query Match 5.2%; Score 80.5; DB 2; Length 408;
Best Local Similarity 20.4%; Pred. No. 0.67;
Matches 59; Conservative 44; Mismatches 91; Indels 95; Gaps 17;

OY 15 TGFYNRIVLSHLLPANLWEPRLPHFLQTLWRNYLAGTLLYFISGFLMCF-----YIY 65
DB 148 YGFYTLAIADFL-----FCVT-----LPFKIAYHLNNGNMNVFGEVLCRATTYVF 192
OY 66 YKINIVYLPKDAIPTKAMRLQMFVAMKAMPYTLTPYSESIIEGKTKCFASIDEPFG 125
DB 193 Y--GNNYC--SILLACISINRYLAIVHPFTYRGIPKHTYALVTCGLV-----W 237
OY 126 IYFVYIAIYLVFVEFGIYMMHRELHDIPKYKYLATHHINYKONTLSP-----PAGLA 180
DB 238 ATVFYLMPLPFI-----LKOEYLVQP--DITTCADVHTCCSSSPFOLYITISLA 286
OY 181 FHPVDGIIQAVPHVIALFTVPIHFTTHIGLLEMEAIWTANIHDCIIGNTPVYGA----- 235
DB 287 FE---GFL--IPFVLIIY-----CYAAIIRTLNAYD--HRMLWYVVASLIIIV 327
OY 236 -----GYHTIHTTYKHN--GYHTIMMDMM-FGSLR--DPL 268
DB 328 IFTICFAPSNIILIIHANYNNMDGLFTYLIALCLDSLNSCLDPFL 376

RESULT 9

US-08-597-236-11

; Sequence 11, Application US/08597236

; Patent No. 5733765

; GENERAL INFORMATION:

; APPLICANT: STINGELE, Francesca

; APPLICANT: MOLETT, Beat

; TITLE OF INVENTION: LACTIC BACTERIA PRODUCING

; TITLE OF INVENTION: EXOPOLYSACCHARIDES

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americans

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/597,236

; FILING DATE:

; CLASSIFICATION: 426

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: EP 95201669.9

; FILING DATE: 20-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Panucci A., Allan

; REGISTRATION NUMBER: 30256

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 360 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-597-236-11

Query Match 5.1%; Score 80; DB 1; Length 360;
Best Local Similarity 18.5%; Pred. No. 0.64;
Matches 46; Conservative 35; Mismatches 58; Indels 110; Gaps 12;

OY 14 ETSFYNRIVLSHLLPANLWEPRLPHFLQTLWRNYLAGTLLYFISGFLMCFYIY-LKINIV 72
DB 94 EITFANSVLITITIGIPKVAEH-----YFVATPLYLSLFYVATSFNI- 137
OY 73 LRPDAIPTKAMRLQMFVAM-----KAMPWY--TLTPVYBSMSIERGWTKCF 117
DB 138 -----SROFIAGLVLAISFALDKKMPWMLITVLATLFA----- 174
OY 118 ASIDFGWILYFYVYIAIYLVFVEFGIYMMHRELHDIPKYKYLATHHINYKONTLSPRA 177
DB 175 -----TAIVAFPYWLTQVMDVK-----KTLISF-----PITIRA 205
OY 178 GLAFHPVDGI-LQAVPH-----VIALEFVPIHFTTHIGLLEME 215
DB 206 SEIFDAIILNIFVFPFHYEMVINGTOFNISDQCGRVAVLKIPILDLFTL---FLFYKK 262
OY 216 IWTANTHDC 224
DB 263 SY-ALISEC 270

RESULT 10
US-08-746-682A-11
; Sequence 11, Application US/08746682A
; Patent No. 5786184
; GENERAL INFORMATION:
; APPLICANT: STINGELE, Francesca
; APPLICANT: MOLETT, Beat
; TITLE OF INVENTION: LACTIC BACTERIA PRODUCING

Mon Apr 8 17:54:17 2002

us-09-775-879-21.raii

Page 7

NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 STREET: 1100 NEW YORK AVE.,
 CITY: WASHINGTON, NM, SUITE 600
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/467,947A
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/04079
 FILING DATE: 30-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: STEEFE, ERIC K.
 REGISTRATION NUMBER: 36,688
 REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 29:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 325 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: not relevant
 MOLECULE TYPE: peptide
 OS-08-467-947A-29

Query Match	4.98;	Score	76.5;	DB	3;	Length	325;
Best Local Similarity	22.78;	Pred. No.	1.4;				
Matches	44;	Conservative	36;	Mismatches	73;	Indels	41;
						Gaps	11

```

QY 5 NALMAGVDEDSFFNRIVLSHLLPRANLMEPLPHLQWLNRNYLAGTLLYFISGLMCFYI 64
      1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1:
Db 2 NSTSTQPPDESCSONLLITQOIPV-----LYCWVFIAGILLNGVSG--WTF- 47
      1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1:
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RESULT 13
 US-08-988-876--8
 : Sequence 8, Application US/08588876
 : Patent No. 6063596
 : GENERAL INFORMATION:
 : APPLICANT: Lal, Preeti
 : APPLICANT: Bandman, Olga
 : APPLICANT: Hillman, Jennifer L.
 : APPLICANT: Yue, Henry
 : TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
 : WITH IMMUNE RESPONSE
 : NUMBER OF SEQUENCES: 9
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Incyte Pharmaceuticals, Inc.
 : STREET: 3174 Porter Drive

CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastEO for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/988,876
 FILING DATE: Herewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0441 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEFAX: 650-845-4166
 TELEX:
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 338 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 285955
 US-08-988-876-8

Query Match	4.9%;	Score 76.5;	DB 3;	Length 338;
Best Local Similarity	22.7%;	Pred. No. 1.5;		
Matches 44;	Conservative 36;	Mismatches 73;	Incls 41;	Gaps 11;

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QY      182  HPVDSGLIQAVPHVI  195
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RESULT 14
 US-09-303-524A-2
 : Sequence 2, Application US/09303524A
 : Patent No. 6238873
 : GENERAL INFORMATION:
 : APPLICANT:
 : APPLICANT: CHAMBERS, JONATHAN K. .
 : APPLICANT: STEWART, BRIAN R.
 : APPLICANT: AMES, ROBERT S.
 : APPLICANT: SARAG, HENRY M.
 : APPLICANT: POLEY, JIM
 : APPLICANT: ARNOLD, ANNE ROMANIC
 : TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
 : TITLE OF INVENTION: ANTAGONISTS OF THE INTERACTION BETWEEN THE HUMAN KIAA0001
 : TITLE OF INVENTION: RECEPTOR AND LIGANDS THEREOF
 : FILE REFERENCE: GP50007

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 4, 2002, 17:05:11 ; Search time 23.17 Seconds

(without alignments)
898.342 Million cell updates/sec

Title: US-09-775-879-21

Perfect score: 1562
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Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1020	65.3	333	22	AA680924	Sterol C5 desaturase
2	771	49.4	136	21	AA628356	Arabidopsis thaliana
3	716	45.8	148	21	AA618089	Eucalyptus grandis
4	606	38.8	139	21	AA628354	Arabidopsis thaliana
5	566	36.2	131	21	AA628355	Arabidopsis thaliana
6	330	21.1	307	21	AA656950	Human prostate can
7	172	11.0	266	21	AA616769	Arabidopsis thaliana
8	167	10.7	252	21	AA641385	Arabidopsis thaliana
9	167	10.7	253	21	AA641384	Arabidopsis thaliana
10	164.5	10.5	177	21	AA641386	Arabidopsis thaliana
11	158.5	10.1	173	21	AA616771	Arabidopsis thaliana

12	158.5	10.1	183	21	AA616770	Arabidopsis thaliana
13	158.5	10.1	211	21	AA624357	Arabidopsis thaliana
14	158.5	10.1	220	21	AA624356	Arabidopsis thaliana
15	158.5	10.1	221	21	AA624355	Arabidopsis thaliana
16	148.5	9.5	293	18	AA614481	Rattus ra
17	147.5	9.4	265	21	AA698034	Rice SYR2 homologue
18	141.5	9.1	625	18	AA618008	Arabidopsis CER1 P
19	140.5	9.0	206	21	AA607244	Arabidopsis thaliana
20	140.5	9.0	206	21	AA650821	Arabidopsis thaliana
21	140.5	9.0	214	21	AA607243	Arabidopsis thaliana
22	140.5	9.0	214	21	AA650820	Arabidopsis thaliana
23	140.5	9.0	298	21	AA607242	Arabidopsis thaliana
24	140.5	9.0	298	21	AA650819	Arabidopsis thaliana
25	138.5	8.9	580	21	AA630495	Arabidopsis thaliana
26	138	8.8	211	21	AA631068	Arabidopsis thaliana
27	138	8.8	219	21	AA631067	Arabidopsis thaliana
28	138	8.8	303	21	AA631066	Arabidopsis thaliana
29	137	8.8	310	21	AA657936	Human transmembran
30	136.5	8.7	258	21	AA698033	Corn SYR2 homologue
31	135.5	8.7	625	21	AA603108	Arabidopsis glossy
32	135	8.6	259	21	AA698035	Soybean SYR2 homol
33	135	8.6	264	21	AA698032	Corn SYR2 homologue
34	130.5	8.4	210	21	AA618064	Pinus radiata meth
35	130.5	8.4	452	21	AA630496	Arabidopsis thaliana
36	129	8.3	301	21	AA638120	Arabidopsis thaliana
37	129	8.3	339	21	AA638119	Arabidopsis thaliana
38	127	8.1	161	21	AA698030	Arabidopsis thaliana
39	126	8.1	234	21	AA606732	Arabidopsis thaliana
40	124	7.9	217	21	AA638121	Arabidopsis thaliana
41	123.5	7.9	216	21	AA698037	Wheat SYR2 homolog
42	123	7.9	269	21	AA698036	Wheat SYR2 homolog
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ALIGNMENTS

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KW	Moss: Physcomitrella patens; lipid metabolism related protein; LMPB;
KW	lipid biosynthesis; lipid modification; lipid degradation; cofactor;
KW	fatty acid transport; genetic engineering; fatty acid; enzyme; plant;
KW	microorganism; polyunsaturated fatty acid; oilseed plant; maize; wheat;
KW	biotic stress tolerance; abiotic stress tolerance; rice; oat; triticale;
KW	rice; barley; soybean; peanut; cotton; rapeseed; canola; manihot;
KW	pepper; sunflower; tagetes; potato; tobacco; eggplant; tomato; vicia;
KW	pea; alfalfa; coffee; cacao; tea; Salix; oil palm; coconut;
KW	perennial grass; forage crop.
XX	XX
OS	Physcomitrella patens.
XX	XX
PN	WO200138484-A2.
XX	XX
PD	31-MAY-2001.
XX	XX
PF	22-NOV-2000; 2000WO-EP11615.
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PR	25-NOV-1999; 99WO-EP09108.
XX	XX
PA	(BADT) BASF PLANT SCI GMBH.
XX	XX
PI	Lerchl J, Renz A, Ehrhardt T, Reinold A, Cirpus F, Bischoff F;
PI	Frank M, Freund A, Duwenig E, Schmidt R, Reski F;

PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
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Best Local Similarity 100.0%; Pred. No. 1.3e-80;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AC AAB18089;
XX 08-NOV-2000 (first entry)
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KW metabolism; isoprenoid biosynthetic pathway; terpenoid; steroid;
KW genome mapping; physical mapping; positional cloning; forestry;
KW agriculture; medicine; fermentation; plant development; pest resistance;
KW pinene; myrcene; Monterey pine.
XX
OS Eucalyptus grandis.
XX
XX
PN WO200036081-A2.
XX

[illegible]

XX	Arabidopsis thaliana.	
OS	Arabidopsis thaliana.	
PN	EP1033405-A2.	
PD	06-SEP-2000.	
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Query Match 38.8%; Score 606; DB 21; Length 139;
Best Local Similarity 93.5%; Pred. No. 1.2e-61;
Matches 115; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1 MADNAYLMQFVDETSFYRRIYLSHLLPANLMEPLPHFIQTWLRNYIAGTLTYFISGFLM 60
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Db 1 maadnaylmqfvdetsfyrrivlsllpanlmeplphfiqtwlrnyjagtllyifsgflw 60
|||||

OY 61 CFYIYKLTINVLPKDAITPTIKAMRLQMFVANKAMPWYTLPTVSESMTERGWTCKCFASI 120
|||||
Db 61 cfyiykltinvyllpkdaipctikamrlqmfvankampwyltlptvse:mlterxwckcfasi 120
|||||

OY 121 DEF 123
||
Db 121 get 123

RESULT 5
AAG28355
ID AAG28355 standard; Protein; 131 AA.
XX
AC AAG28355;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 33542.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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XX Arabidopsis thaliana.
OS
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
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Query Match 36.2%; Score 566; DB 21; Length 131;
 Best Local Similarity 93.0%; Pred. No. 4, 5e-57;
 Matches 107; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY 9 MOFVETSEFYNRIVLSHLPLANLMEPLPHFLQTWLRNLTAGTLTYFISGFLMCFYIYLYK 68
DB 1 mqvfetstfynrlvslshllpanlweplphflqtlwlrnltagtltyfissgflmcfyiylyk 60
QY 69 INVYLPKDAIPITKAMRLQMFVAMKAMPWYTLPLVSESMIERGWTGCFASIDEF 123
DB 61 InvYLPkDAIPITkAMrLQmFvAMkAMpWtLPLvSeSmIErGwTgCfASIdEf 115

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RESULT 6
 AAB56950
 ID AAB56950 standard; Protein; 307 AA.

AC AAB56950;
 XX
 DT 13-MAR-2001 (first entry)

DE Human prostate cancer antigen protein sequence SEQ ID NO:1528.

XX Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
 KW neuroprotective; cytosolic; cardioactive; immunomodulatory; muscular;
 KW vulnery; gastrointestinal; nephrotropic; antinefective; gynaecological;
 KW antibacterial; gene therapy; neural; immune; reproductive; renal;
 KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
 KW wound; infectious disease.

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XX Homo sapiens.
OS
XX WO200055174-A1.
PN
XX
XX 21-SEP-2000.
PD
XX
XX 08-MAR-2000; 2000MO-US05988.
XX
XX 12-MAR-1999; 99US-0124270.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
XX PI Rosen CA, Ruben SM;
XX WPI: 2000-587513/55.
DR N-PSDB; AAF16153.
XX
XX Prostate cancer associated gene sequences, referred to as prostate
PT cancer antigens, useful for treatment, prevention, and diagnosis of
PT disorders such as prostate cancer -
XX
XX Claim 11; Page 1969-1970; 2338pp; English.
PS
XX AAF15566 to AAF16505 encode the human prostate cancer associated
CC proteins, called prostate cancer antigens, given in AAB57302.
CC The prostate cancer antigens can have neuroprotective, cytosolic,
CC cardioactive, immunomodulatory, muscular, vulnery, gastrointestinal,
CC nephrotropic, antinefective, gynaecological and antibacterial activities,
CC and can be used in gene therapy. The prostate cancer antigen
CC polynucleotides may be used for detection of prostate cancer, chromosome
CC identification, as chromosome markers, and for numerous other diagnostic
CC or research purposes. The prostate cancer antigens may be used to treat
CC disorders such as neural, immune, muscular, reproductive,
CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC AAB53303 represent sequences used in the exemplification of the present
CC invention.
XX
XX Sequence 307 AA;
SQ

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Query Match 21.1%; Score 330; DB 21; Length 307;
 Best Local Similarity 32.9%; Pred. No. 2e-29; 73; Indels 42; Gaps 12;
 Matches 82; Conservative 52; Mismatches 73; Indels 42; Gaps 12;

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QY 51 LLYFISGFLMCFYIY-----YLKINVYLPKDAIPITKAMRLQMFVAMKAMPWYTL 101
DB 45 llyfcaatlssyfvfdhalmkhpqflkngy-----rrel:ftvgalpwlsil 91
QY 102 PLYSESMIE-RGWTGCFASIDERGWLTYFYNAI--YLVFVEGCIWHIRELHDIPLYK 158
DB 92 -lvallllslrsgsklhdldgefyglfelvvalisflfftdmfiyw:hngllh-lyvk 149
QY 159 YLCHATHIYNKQWTLSPFAGLAFHPVDGIQANPHVIALFTVPIHPT:HTGLFMEAIWT 218
DB 150 rlhkphniw---klrpfashahpdpdglfqs:lpynlhpflfipbhvw:ylsilylwniwt 206
QY 219 ANIHDCIHGN-----IWP-VMGAGYHTHTHTYKKNYGHY-TIMWDIMEGSIRDLLEE 270
DB 207 lsihd---gdfirvpqllqpfingsahhtdhmfdfdyngyftlw-d:lgsgfkpsste 262
QY 271 DDNKDSFKK 279
DB 263 gkgplsyvk 271

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RESULT 7
 AAG16769
 ID AAG16769 standard; Protein; 266 AA.
 AC AAG16769;

XX 17-OCT-2000 (first entry)
DT Arabidopsis thaliana protein fragment SEQ ID NO: 17541.
XX
DE
XX Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
OS Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
PD
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
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 DT 18-OCT-2000 (first entry)
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 KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
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Db	86	fmgme-----ssfr-----lps-----	wkvsaqdlfgyfliedfv	115
QY	143	IYVMHRELNDIKPLKYKYLHATNTIYNKONTLSPPA-----	GLAFHPYDGLQA	190
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KW	Protein identification; signal transduction pathway; metabolic pathway;			
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Pr 178 -----GLAHPRDGILQANPHVIAEFIVPINFHTNHGILFEMAIWTANIHDCIH-----	227					
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KM Protein identification; signal transduction pathway; metabolic pathway;						
KW hybridisation assay; genetic mapping; gene expression control; promoter;						
KW termination sequence.						
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 4, 2002, 22:35:46 ; Search time 3635.3 Seconds

(without alignments)
8572.380 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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36: em_htg_other: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1876.4	99.3	3004	8	AF069468	AF069468 Arabidops
3	1876.4	99.3	103904	8	AFAC021640	AFAC021640 Arabidops
4	486.6	25.8	1175	8	AFRNASC5D	X90454 A.thaliana
5	269.2	14.3	138711	8	AFPO03214	AFPO03214 Oryza sat
6	186.2	9.9	1155	8	AF081794	AF081794 Nicotiana
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8	164.2	8.7	1381	6	AX155063	AX155063 Sequence
9	132.2	7.0	313	11	G71612	G71612 A62988234FM
10	128.4	6.8	293	11	G71681	G71681 A85715834FM
11	60	3.2	7218	8	I66494	I66494 Sequence 14
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13	57.4	3.0	696	8	CNS018D5	AL114081 Botrytis
14	56.6	3.0	1721	10	AB016248	AB016248 Mus muscu
15	56.6	3.0	127709	2	CNS05FC1	AL352983 Homo sapi
16	55.8	3.0	52359	2	AC010772	AC010772 Homo sapi
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ACCESSION	AF105034				
VERSION	AF105034				
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SOURCE					
ORGANISM					
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	Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.				
REFERENCE	1 (bases 1 to 2294)				
AUTHORS	Choe,S., Noguchi,T., Fujioka,S., Takatsuto,S., Tisler,C.P.,				
	Gregory,B.D., Ross,A.S., Tanaka,A., Yoshida,S., Txx,F.E. and				
	Feldmann,K.A.				
TITLE	The Arabidopsis dwf7/stel mutant is defective in the delta7 sterol				
JOURNAL	C-5 desaturase step leading to brassinosteroid biosynthesis				
	Plant Cell 11 (2), 207-221 (1999)				

MEDLINE 99128169
PUBMED 9927639
REFERENCE 2 (bases 1 to 2294)
AUTHORS Choe,S., Tanaka,A., Gregory,B.D. and Feldmann,K.A.
TITLE Direct Submission
JOURNAL Submitted (06-NOV-1998) Plant Sciences, The University of Arizona,
Forbes Hall 303, Tucson, AZ 85721, USA
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DB 61 TGTTCATTAAGTAAGTAAGTAAGTAATCCGGCAATCTTCTTTCGTTTCCGGCACC GA 120
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QY 241 accctaccatcttttccagacatgagtcggaatctactcgcggaaccctacata 300
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VERSION	AF069468.1	GI:4234767			

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ORGANISM	Arabidopsis thaliana Eunaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots; Rosidae; eurosids II: Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 3004)
REFERENCE	Husselstein,T., Schaller,H., Gachotte,D. and Benveniste,P. Delta ⁸ -sterol-C5-desaturase: molecular characterization and functional expression of wild-type and mutant alleles Plant Mol. Biol. 39 (5), 891-906 (1999) 99273392
AUTHORS	2 (bases 1 to 3004)
TITLE	Husselstein,T., Schaller,H., Gachotte,D. and Benveniste,P. Direct Submission Submitted (30-MAY-1998) IEMP, 28, rue Goethe, Strasbourg 67083, France
JOURNAL	
MEDLINE	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	

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 QY 1860 taaacaatgaatgttctgactcttcg 1889
 Db 2960 TAAACATGTAATGTTTGATGATCTTTC 2989

REFERENCE
 AUTHORS
 Lin, X., Kaul, S., Town, C. D., Beilto, M., Greasy, T. H., Haas, B., Wu, D., Bowman, C. L., White, O., Nierman, W. C., and Fraser, C. M.
 Arabidopsis thaliana chromosome III BAC F16B3 genomic sequence
 Unpublished
 2 (bases 1 to 103904)
JOURNAL
 TITLE
 Lin, X. and Kaul, S.
 Direct Submission
 Submitted (18-JAN-2000) The Institute for Genomic Research, 9712
 Medical Center Dr., Rockville, MD 20850, USA, xlin@tigr.org
 3 (bases 1 to 103904)
REFERENCE
 AUTHORS
 TITLE
 Lin, X.
 Direct Submission
 Submitted (24-JAN-2001) The Institute for Genomic Research, 9712
 Medical Center Dr., Rockville, MD 20850, USA
 On Jan 24, 2001 this sequence version replaced g1:12280770.
 Address all correspondence to: at@tigr.org

COMMENT
 BAC clone F16B3 is from Arabidopsis chromosome III and is near the
 molecular marker m174.
 The orientation of the sequence is from SP6 to T7 end of the BAC
 clone.
 Genes were identified by a combination of three methods: Gene
 prediction programs including GAIL (available by anonymous ftp
 from arthur.epm.ornl.gov), GeneFinder (Phil Green, University of
 Washington), Genscan (Chris Burge,
 http://www.cbs.dtu.dk/netgene/cbsnetgene.html), and NetPlantGene
 (http://www.cbs.dtu.dk/netgene/cbsnetgene.html), searches of the
 complete sequence against a peptide database and the Arabidopsis
 EST database at TIGR (http://www.tigr.org/db/at.html).
 Annotated genes are named to indicate the level of evidence for
 their annotation. Genes with similarity to other proteins are named
 after the database hits. Genes without significant peptide
 similarity but with EST similarity are named as 'unknown' proteins.
 Genes without protein or EST similarity, that are predicted by more
 than two gene prediction programs over most of their length are
 annotated as 'hypothetical' proteins. Genes encoding tRNAs are
 predicted by tRNAscan-SE (Sean Eddy,
 http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are
 identified by RepeatMasker (Arjan Smit,
 http://ftp.genome.washington.edu/RM/RepeatMasker.html).
 Location/Qualifiers

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RESULT 4
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LOCUS ATRNASC5D 1175 bp mRNA PLN 13-FEB-1997
DEFINITION A.thaliana mRNA for sterol-C5-desaturase.
ACCESSION X90454
VERSION X90454.1 GI:1061037
KEYWORDS sterol-C5-desaturase gene.
SOURCE
ORGANISM Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots;
Rosidae: eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1175)
Gachotte,D., Husselstein,T., Bard,M., Lacrouse,F. and Benveniste,P.
Isolation and characterization of an Arabidopsis thaliana CDNA
encoding a delta 7-sterol-C-5-desaturase by functional
complementation of a defective yeast mutant
Plant J. 9 (3), 391-398 (1996)
97077348
JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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BASE COUNT 300 a 265 c 227 g 383 t
ORIGIN

Query Match 25.8%; Score 486.6; DB 8; Length 1175;
Best Local Similarity 98.2%; Pred. No. 2.3e-93;
Matches 492; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Db 1123 TAAATGTTGATGATCTTTC 1143

RESULT 5
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LOCUS Oryza sativa genomic DNA, chromosome 1, BAC clone: OSUNBA0083M16,
DEFINITION complete sequence.
ACCESSION AP003214
VERSION AP003214.2 GI:13620983
KEYWORDS HTG.
SOURCE Oryza sativa (cultivar: Nipponbare) DNA, clone: OSUNBA0083M16.
ORGANISM Oryza sativa

REFERENCE
AUTHORS Sasaki, T., Matsumoto, T. and Yamamoto, K.
TITLE Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
JOURNAL clone: OSUNBA0083M16
PUBLISHED Only in Database (2001) In Press
2 (bases 1 to 138711)
AUTHORS Sasaki, T., Matsumoto, T. and Yamamoto, K.
TITLE Direct Submission
JOURNAL Submitted (19-FEB-2001) Takuji Sasaki, National Institute of
Agrobiological Resources, Rice Genome Research Program, Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail: tsasaki@abr.affrc.go.jp, URL: http://rpg.dna.affrc.go.jp/,

Tel: 81-298-38-7441, Fax: 81-298-38-7468)
On Apr 12, 2001 this sequence version replaced gi:13027244.
The orientation of the sequence is from -21M13 to M13rev of the BAC
clone.

FEATURES
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BASE COUNT 37474 a 31378 c 32147 g 37712 t
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Query Match 14.3%; Score 269.2; DB 8; Length 138711;
Best Local Similarity 57.7%; Pred. No. 2.9e-47;
Matches 548; Conservative 0; Mismatches 383; Indels 19; Gaps 3;

OY 727 ttgtctgagatgcaattccttaacaaagagctatgctgttgaatgttgtgcaatgta 786
Db 90614 TTGATGAGATTCTATACCTACATCGAAGCTATGAAAGAAATTAATGTTGCTGATCAA 90673
OY 787 aagcatccaatggtacactctcttccaaactgctccgagaagtatga-tgaacgtggt 846
Db 90674 AGGCTATGCTCTCTATTTGTGCTTCCACCTTATCTAGTACATGCTTGGAATGAT 90733
OY 847 ggaaccaaatgtttgtcagacagaaatcgcgtgagatctglatl-tgttcaatcg 906
Db 90734 GGACACAGCTTATGTTATATACAGTAAGAGTGTGGCCAAATGTAACCTGGTTTATCTCG 90793
OY 907 ccatcatctgttttctgtgtgtgtgtgtatattatgttgatgacagagtgctcatgaca 966
Db 90794 CTTTATATCTTATCTTGTGTTGAGTTGGAATTTACTGATGACAGAGTGTGATGACA 90853
OY 967 ttaagcctctcatalagatctccatgcccacccaatcatalctcaacaagaaataaac 1026
Db 90854 TAAACCAATGTGTACAGATACGACACATACCATATTTTACAAACAGCAATACCC 90913
OY 1027 tctctccattgctcggaagtgt-----ttcaagttgttcttcttcttct 1074
Db 90914 TATCACCAATTTGACAGTAAATTTTATGAGCCGCTTATATATGCAATTCATTTTAA 90973
OY 1075 tctaaagaatgttagcatgtttcttaccagaagaacttctgtca-icagctgctgt 1134
Db 90974 TTTTTCGCTGTGCAATGATATATATATGAGACAGATTCATATTCGATVGCCTTATTTT 91033
OY 1135 actccaatcacaatttgcattcctatccataaaglaacagaaag-ctagaatlatat 1194
Db 91034 ACCATGCTTCCAGCTTTTATGATATATCTGTGATATATATATTTCCCTGCTAA 91093
OY 1195 aaatgcaagctgcatcttcaacatatagtcagaagaactctga----ttaacaagagt 1250
Db 91094 TTAATATGCTTAAACACTAGGATACCTTATTTAAGGCTCTTAAACCTTTTACCCGTAG 91153
OY 1251 ttagaatcttgtgttcttcttcttctgtctcgcgactgattggaatagcgtgaagttcttt 1310
Db 91154 CCATACCAATATAAAAAAATGCAATGCGCTCCCAATGTACATTTTAA--CAATA 91210
OY 1311 atctactccctcgaggtgtatcttctgttaatccaagaagtacatctatatacttgt 1370
Db 91211 CAATTTTCTTATTAACCTCTTTGCTGTGAGAAATGTGATTTCTTCACCAAGCTTCT 91270
OY 1371 aacttcccttaagctttgttcaagagctgcatcttccaccagtagacjgtaactcag 1430
Db 91271 GATTTATGCTTGTGCAATGCTTCCAGAGACTAGCATTCATCCATGATGGATTTTGGCAA 91330
OY 1431 gctgtacagcaatgtagcgtgtttatagcgaatcattcattacaactatagtagt 1490
Db 91331 GCCATACCGCATGTGTTGCTGTACCTTATCCCAACACACTTCAGGACACACATGTGT 91390
OY 1491 ctltgttcatggaagcagatagcagcaacatcattgactgtatc-actgcaacatc 1550
Db 1550 ctltgttcatggaagcagatagcagcaacatcattgactgtatc-actgcaacatc 1550

Df	91391	CCTGTTGCATGTAGAGGCCGTGTGGACAACATAACATCCATGACTGATTCACGGCAAGCTT	91450
Oy	1551	tggccagtaabtggtgtgcaggatatacctacgatatcaaccacagacatacacaagtactat	1610
Dd	91451	TGGCGTGTCATTATGGTGTGGCTGTATGCACACCATTCCACATACAACTACCGTCGTCACATAT	91510
Oy	1611	ggctcatatcacatbtgatgatgtggatgttcttgaccttccttaggaacc	1660
Dd	91511	GCCCATCACACCCTGTGTGATGAGTAGTGATGTTCGGCACCCTTCGAGAGCC	91560
RESULT	6		
LOCUS	AF081794	AF081794	1155 bp mRNA PLN 19-MAY-1999
DEFINITION	Nicotiana tabacum sterol-C5(6)-desaturase mRNA, complete cds.		
ACCESSION	AF081794		
VERSION	AF081794.1	GI:4140397	
KEYWORDS			
SOURCE	Common tobacco.		
ORGANISM	Nicotiana tabacum		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.		
AUTHORS	1 (bases 1 to 1155)		
TITLE	Husselstein,T., Schaller,H., Gachotte,D. and Benveniste,P.		
JOURNAL	Delta7-sterol-C5-desaturase: molecular characterization and functional expression of wild-type and mutant alleles		
MEDLINE	Plant Mol. Biol. 39 (5), 891-906 (1999)		
REFERENCE	99273992		
AUTHORS	2 (bases 1 to 1155)		
TITLE	Benveniste,P.		
JOURNAL	Direct Submission		
	Submitted (30-JUL-1998) Plant Molecular Biology Institute, Centre National de la Recherche Scientifique, 28 rue Goethe, Strasbourg 67084, France		
FEATURES	Location/Qualifiers		
source	1..1155		
	/organism="Nicotiana tabacum"		
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	/rfeature_type="calli derived from leaf protoplasts"		
	103..918		
	/codon_start=1		
	/product="sterol-C5(6)-desaturase"		
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	/db_xref="GI:4140398"		
	/translation="MEDYKQFVEETSFYNRLVLTGPMSWCPRLPHMLQGILNRTI GGVLFTSGFLGCFITLHKRNVTIRKDAIPSKAMLDIVAKMPWCALPSLS EYMENQNTKCFARISDVGVSLTYVALVLYEFITVMHMLNDIKELYLIANT HHHNKNQLSPFGAFAHFHPDLGTLQAVPVALLLVPMEHTIALIFLEALTANI HDCIHGVFPVMGAGYTHIHRTYRHNHYTIWMDMFGTRLRPVEDAKM"		
CDS			
BASE COUNT	310 a 239 c 245 g 361 t		
ORIGIN			
Query Match	9.9%; Score 186.2; DB 8; Length 1155;		
Best Local Similarity	72.2%; Pred. No. 1.5e-29;		
Matches 242:	Conservative 0; Mismatches 93; Indels 0; Gaps 0;		
Oy	720	gtctgttttgtctcgatgagaatctctcataaagaagcgtatgcgttgcgaatgttctg	779
Dd	304	GTAATATTTCTGAAGAAGGACCATCCCTTTCAACAAGAAGCTCTTCCAATATACAGTA	363
Oy	780	gcaatgaagcgtatgcatactgttacactctctccaactgtctctccgagatgatgaa	839
Dd	364	GCCATGAAGCGATGCCATGTACTGTGCTCCCTTCATCATTTTCTGAGTACATATTTAA	423
Oy	840	cgtgttgcaccaaatgttctgtcagcatagacgaatccggtcgttatctgtatttct	899
Dd	424	AATGATGTGACAAAATGTTTTCAGAGATTAAGTATGATGTGTGATGCTTCTATGTATTC	483
Oy	900	tacatgccatcatctgttctgttgaagtttgtattatattatgatatgcacagagctt	959

[illegible]

Db 448 AATGGGTGACAAAATGTTCTCAAGAAATTCAGCGATTGGATGGCTTCTACCTTAT 507
 Oy 900 tacatcgccatcatctgttctgttgatgttgatattatgtagacagaagctt 959
 Db 508 TATATGGCAGTTATTTGGTAATAGATATTCGGCATTCTGATGATGATGCGAGTTG 567
 Oy 960 catgacatlaagcctctatlaagatctcctacgacccatcatatctacaagaagcag 1019
 Db 568 CATGACATAAACCTCTGTACAAATATCTCCATGCTACACATCATATTTACAAACAA 627
 Oy 1020 aatacactctccatcttgcggtgaagtcttca 1054
 Db 628 AATACACTCTCCCATTTGCTGGTTGGCTTCCA 662

RESULT 8
 AX155063 1381 bp DNA PAT 22-JUN-2001
 LOCUS AX155063
 DEFINITION Sequence 109 from Patent WO0138484.
 ACCESSION AX155063
 VERSION AX155063.1 GI:14536617
 KEYWORDS
 SOURCE Physcomitrella patens.
 ORGANISM Physcomitrella patens
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
 1 (bases 1 to 1381)
 REFERENCE Lerch, J., Renz, A., Ehrhardt, F., Reindl, A., Citpus, P., Bischoff, F.,
 Frank, M., Freund, A., Duenweg, B., Schmidt, R. M. and Reski, R.
 Moss genes from Physcomitrella patens encoding proteins involved in
 the synthesis of polyunsaturated fatty acids and lipids
 Patent: WO 0138484-A 109 31-MAY-2001;
 BASF Plant Science GmbH (DE)
 JOURNAL Location/Qualifiers
 FEATURES
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 /organism="Physcomitrella patens"
 /db_xref="taxon:3218"
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 /note="p004064012R"
 /codon_start=1
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 GAKTSGGVANGSPYIALFVEETRWYNDVLGPMPLSSVRDIPTLTQMLNRY
 AGMLYFSGSLWCTLYYSKMGHEFPAGDIIPAKPIMLQIMTMKADPVYTGIDPIS
 EYMERGWTKCFARIEDYGMILTYGVYATYAVYFEGYIMHRELDHDKPLKHLHAT
 HHTYKQNTLSFPAGLAHPIDGLDQCPHYIALFLPMHFTEHVLLEFCGVTNTI
 HDCIDGVNWMGIMGAFTHHTYRHNGHYTFMDLFTLRDPYERKATAHVKS"
 BASE COUNT 323 a 331 c 351 g 376 t
 ORIGIN

Query Match 8.7%; Score 164.2; DB 6; Length 1381;
 Best Local Similarity 68.7%; Pred. No. 6.8e-25;
 Matches 226; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

Oy 726 ttgtcttgcagtcgaatccctacataaagctatgctgttgcaaatgtttggaagc 785
 Db 421 TTCCCTGACGGTACCATACCCGCGAAGAGCCCAATATGCTCAATCTGGGTATAG 480
 Oy 786 aagcgtatgcataagctatctctccaaactgtctcgaagatgataaagctgtg 845
 Db 481 AAGGCTATGCCAGTATACAGAGACTTCCCACTCTGTCGCAATATATGATTGAGCGGGG 540
 Oy 846 tggaccaaagtcttctgtagcagaatcgctgagatctgattatttgaacatc 905
 Db 541 TGGACCAAGTGTTCGCGCATCGAGATGTTGGTGTCTACGATGATAGCGCTAGTC 600
 Oy 906 gccatctatctgtttgttgatgttatattatgtagcagaagaagattatgc 965
 Db 601 ATCCGCTACTTGCGAGCTGTGAGATTGTGATCTATGGATCCACGAGAGCTTACGAT 660
 Oy 966 ataagcctctctataaglatctccatgccaaccatcatatctacaagaagataata 1025

Db 661 ATTAAGCCCTTTGTAACAACATCTGCATGCTACCCACACACTTACATATAGCAAAACAGC 720
 Oy 1026 cctctccatctgcggtgaagtcttca 1054
 Db 721 CTATCACCGTTTGACAGTTTGGCGTTCCA 749

RESULT 9
 G71612/c 310 bp DNA STS 08-JUN-2001
 LOCUS G71612
 DEFINITION A62988234FM017 maize leaf DNA Zea mays STS genomic, sequence tagged
 site.
 ACCESSION G71612
 VERSION G71612.1 GI:14333297
 KEYWORDS STS.
 SOURCE Zea mays.
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 310)
 REFERENCE Yang, Y. J., Guo, L., Ashlock, D. A., Wen, T. J. and Schnable, P. S.
 3' UTR sequences of maize genes
 Unpublished
 JOURNAL
 COMMENT

Contact: Schnable, P. S.
 Schnable Laboratory
 Iowa State University
 6405 Agronomy Hall, Ames, IA 50011, USA
 Tel: 515-294-0975
 Fax: 515-294-2299
 Email: schnable@iastate.edu
 Primer A: CTAAATGACACCAAGCC
 Primer B: GATGATATTCGACAGCG
 PCR profile:
 Denaturation: 94 degrees C for 30 seconds
 Annealing: 60 degrees C for 45 seconds
 Polymerization: 72 degrees C for 90 seconds
 PCR cycles: 31
 Thermal cycler: Perkin Elmer TC
 Protocol:
 Template: 10-20 ng
 Primer: each 0.5 uM
 dNTPs: each 200 uM
 Taq polymerase: 0.05 units/uL
 Total vol: 20 uL
 Buffer:
 MgCl2: 2 mM
 KCl: 50 mM
 Tris-HCl: 20 mM
 pH: 8.4.
 FEATURES
 source 1..310
 /organism="Zea mays"
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 /db_xref="taxon:4577"
 /clone_lib="maize leaf DNA"
 /note="PCR products amplified from genomic DNA"
 STS
 BASE COUNT 80 a 81 c 87 g 62 t
 ORIGIN

Query Match 7.0%; Score 132.2; DB 11; Length 310;
 Best Local Similarity 73.0%; Pred. No. 4.5e-18;
 Matches 170; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Oy 1428 cagcgtatccgcatatgtagcgtgttattatagtgcaattcatcttcaactcatata 1487
 Db 309 CAAGCAATGCCGATGCTTGGCTCTCTCTCCCAACGACACTT;AGGACGACATC 250

CNS0180K
LOCUS
DEFINITION Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation.
ACCESSION AL110675.1 GI:5824962
VERSION AL110675
KEYWORDS cDNA library; nitrogen deprivation.
SOURCE Botryotinia fuckeliana
ORGANISM Botryotinia fuckeliana
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes; Helotiales; Sclerotiniaceae; Botryotinia.
REFERENCE
AUTHORS Bilton,F., Lewis,C., Fortini,D., Pradier,J.M. and Brygoo,Y.
TITLE Submitted (01-SEP-1999)
JOURNAL Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr, 78026 Versailles, France
REFERENCE
AUTHORS 2 (bases 1 to 840)
TITLE Direct Submission
JOURNAL Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage : CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT The cDNA library to be analyzed within the framework of this project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBSII vector.
FEATURES
source 1. 840
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/strain="T4"
/db_xref="taxon:40559"
/note="Genoscope sequence ID : W33E091"
BASE COUNT 151 a 23 c 79 g 539 t 48 others
ORIGIN
Query Match 3.0%: Score 57.6; DB 8; Length 840;
Best Local Similarity 46.3%; Pred. No. 0.03; 216; Indels 0; Gaps 0;
Matches 186; Conservative 0; Mismatches 216; Indels 0; Gaps 0;
QY 377 ttccatttgatcactatgcttaacgcgtctcctatgcatcgaatttcaattaa 436
DB 249 TTTTGT 308
QY 437 ggaagagggtcttcgctgctacgtaattggaattgagtgatgcatgct 496
DB 309 TTTTGT 368
QY 497 tgcattatgatatttgcatatctccatcctaaggagttgaacgtagtgctta 556
DB 369 TTTTGT 428
QY 557 tataagtttttgcaaccaacgagagtcgacatcttgaagttgaatttcaactg 616
DB 429 TTTTGT 488
QY 617 ccatttaagtcacctaattgtctgtgaagtgatgctacttcgacacatcttc 676
DB 489 TATATATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 548
QY 677 ttctgctctcgcgactcgtctctgaatctttttgctgcttctgctcaga 736
DB 549 TTTTGT 608
QY 737 tgcattcctacaataaagcgtcgttgcgaatgcttgc 778
DB 609 TTTTGT 650
RESULT 13
CNS0180S

LOCUS
DEFINITION Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation.
ACCESSION AL114081.1 GI:5828700
VERSION AL114081
KEYWORDS cDNA library; nitrogen deprivation.
SOURCE Botryotinia fuckeliana
ORGANISM Botryotinia fuckeliana
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes; Helotiales; Sclerotiniaceae; Botryotinia.
REFERENCE
AUTHORS Bilton,F., Lewis,C., Fortini,D., Pradier,J.M. and Brygoo,Y.
TITLE Submitted (01-SEP-1999)
JOURNAL Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr, 78026 Versailles, France
REFERENCE
AUTHORS 2 (bases 1 to 696)
TITLE Direct Submission
JOURNAL Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage : CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT The cDNA library to be analyzed within the framework of this project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBSII vector.
FEATURES
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/strain="T4"
/db_xref="taxon:40559"
/note="Genoscope sequence ID : W62C051"
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Best Local Similarity 47.5%; Pred. No. 0.034; 187; Indels 0; Gaps 0;
Matches 169; Conservative 0; Mismatches 187; Indels 0; Gaps 0;
QY 377 ttccatttgatcactatgcttaacgcgtctcctatgcatcgaatttcaattaa 436
DB 334 TTTTGT 393
QY 437 ggaagagggtcttcgctgctacgtaattggaattgagtgatgcatgct 496
DB 394 TTTTGT 453
QY 497 tgcattatgatatttgcatatctccatcctaaggagttgaacgtagtgctta 556
DB 454 TTTTGT 513
QY 557 tataagtttttgcaaccaacgagagtcgacatcttgaagttgaatttcaactg 616
DB 514 TTTTGT 573
QY 617 ccatttaagtcacctaattgtctgtgaagtgatgctacttcgacacatcttc 676
DB 574 TTTTGT 633
QY 677 ttctgctctcgcgactcgtctctgaatctttttgctgcttctgctcaga 732
DB 634 TTTTGT 689
RESULT 14
AB016248
LOCUS
DEFINITION Mus musculus mRNA for sterol-C5-desaturase, complete cds.
ACCESSION AB016248
VERSION AB016248.1 GI:3721883
KEYWORDS sterol-C5-desaturase; C5D.
AB016248 1721 bp mRNA ROD 18-FEB-2000


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Db 10196 TTCCCCGATCGTATTGAAATATACNCCCCCGCTGNNNNNNNNNNNNNNNNNNNN 10137
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Db 10136 NNNNNNNNTNNNNNNNTTTTNTNNNTTNTNNNTTNTNNNTTNTNNNTTNTTTT 10077
QY 397 ttgcttaacgccttctatgtlactgaatttcaatttaagaagaagggttcctcgtgt 456
Db 10076 TTTTGTGTTTTTTTTTGTGTTTTTTTTTTTTTTTTNTNTNTNTTTTTTTTTTTNNN 10017
QY 457 actglacagtaacttgaacttgaactgataagtcacgttgcatttacttacttactgt 516
Db 10016 NTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTT 9957
QY 517 gcatattcctcactcaagaagtgacagtgactagtgctatataaagtttltgtcaacca 576
Db 9956 TNNTTTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTT 9897
QY 577 atgaagaagtcgtacaccttgaagtgaaatttctacttgcacattgaagtcacttaaat 636
Db 9896 TTTTNTNTTTTTTTTTTNTTNTTNTTTTTTTTTTTTTTNTTNTTNTTTTTTTTTTTTT 9837
QY 637 tgttltgaaagtgacttgaacttgcagacacatcttcttctcgtctcgtcgaagactct 696
Db 9836 NTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTT 9777
QY 697 gtcttaagttgaacacttlttgcgtcgttcttgccttcagat 737
Db 9776 TTTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTT 9736

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